

SEQUENCE LISTING

<110> Barbet, Anthony F.
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<120> Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, and
Methods of Use

<130> UF-299XC1

<150> US 60/269,944

<151> 2001-02-20

<160> 117

<170> PatentIn version 3.1

<210> 1

<211> 278

<212> PRT

<213> Ehrlichia chaffeensis

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Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
50 55 60

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
65 70 75 80

Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
 100 105 110

Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
 115 120 125

Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
 130 135 140

Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
 145 150 155 160

Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
 165 170 175

Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
 180 185 190

Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
 195 200 205

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
 210 215 220

Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
 225 230 235 240

Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
 245 250 255

Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
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Gly Gly Arg Phe Asn Phe
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<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 aaaaaaactt ttttgtaaat agtcatatta atataacttt tagcaatata aatattgaat 4260
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 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <222> (1)..(372)
 <223> Complement to SEQ ID NO:2, nucleotides <1..372
 Hypothetical dimethyl adenosine transferase
 Product="lhworfli"

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 tggtgggttc gctatatttc gtaaataaat atctaagca tctgataata tgaattcata 120
 tttaccttga aattctttta taattttatc atgtattggt aataatctac tgtctttctc 180

tatagatatt aatTTTTtag gattctTTTT gagtattgaa taagtcattg taccaagtcc 240
 gggaccaatt tcaataattg aaaaattgct aatgtttcct gcataattaa ctatTTTatc 300
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<210> 4
 <211> 723
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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 <222> (1)..(723)
 <223> Corresponds to SEQ ID NO:2, nucleotides 611..1333
 Hypothetical triosephosphate isomerase
 Product="lhworf2"

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 1 5 10 15
 act ttt tct tcg ttt aca aag gag ctt agt aac cgt tta att aat ata 96
 Thr Phe Ser Ser Phe Thr Lys Glu Leu Ser Asn Arg Leu Ile Asn Ile
 20 25 30
 gaa gat aaa gta aag gta gta tta tgc cca cca ttt att gcg tta tct 144
 Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser
 35 40 45
 act tat gtt aat tgt cca cat aat att aag ttt ggt gga cag aac tgt 192
 Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys
 50 55 60
 tgt tat gta tct agt ggg aag tac act gga gaa att agt gct agt atg 240
 Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met
 65 70 75 80
 tta tat aac tct gga tgt agt tat gta ata gtg ggt cac tct gaa agg 288
 Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg
 85 90 95
 agg agt acg ttt cat gaa act gat cat gat gtt agg tta aaa gct gaa 336
 Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu
 100 105 110
 tgt gcg atc gaa tca gga tta ata cca att att tgt gtt gga gaa act 384
 Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr
 115 120 125

tta cta gat agg gaa aat ggt atg cta aaa gat act tta tta agt caa 432
 Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln
 130 135 140
 tgt agt gaa tct ttt cct aaa aat ggt aag ttt atc ata gca tat gag 480
 Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu
 145 150 155 160
 cca gta tgg gca ata ggg aac aat aaa ata cct tct act gat gta ata 528
 Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile
 165 170 175
 ata gaa gct tta gag att att agg tca tat gat tat gta tct gat atc 576
 Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile
 180 185 190
 ata tat ggt gga gca gta aat cat act aat gta ggt gat att gta agt 624
 Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser
 195 200 205
 atc aat caa ttg tct ggt gtt tta gtt ggt agt gct agt tta gat atg 672
 Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met
 210 215 220
 gag agt ttt ttt aat ata ata tgt agt gct ata aat gtg agg caa agt 720
 Glu Ser Phe Phe Asn Ile Ile Cys Ser Ala Ile Asn Val Arg Gln Ser
 225 230 235 240
 taa 723

<210> 5
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 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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1 5 10 15

Thr Phe Ser Ser Phe Thr Lys Glu Leu Ser Asn Arg Leu Ile Asn Ile
20 25 30

Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser
35 40 45

Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys
50 55 60

Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met
65 70 75 80

Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg
85 90 95

Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu
100 105 110

Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr
115 120 125

Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln
130 135 140

Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu
145 150 155 160

Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile
165 170 175

Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile
180 185 190

Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser
195 200 205

Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met
210 215 220

Glu Ser Phe Phe Asn Ile Ile Cys Ser Ala Ile Asn Val Arg Gln Ser
225 230 235 240

<210> 6
<211> 981
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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<222> (1)..(981)
<223> Corresponds to SEQ ID NO:2, nucleotides 1333..2313
Hypothetical cell surface protein precursor
Product="lhworf3"

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 aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att 96
 Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile
 20 25 30

 tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt 144
 Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly
 35 40 45

 agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc 192
 Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser
 50 55 60

 ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat 240
 Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn
 65 70 75 80

 tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta 288
 Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu
 85 90 95

 gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca 336
 Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala
 100 105 110

 atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca 384
 Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr
 115 120 125

 att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa 432
 Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys
 130 135 140

 ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca 480
 Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala
 145 150 155 160

 atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct 528
 Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala
 165 170 175

 gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat 576
 Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp
 180 185 190

 aat aaa att gat gtg atg gta gat gtt gtt gga cat cct aat gct gca 624
 Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala
 195 200 205

att caa gaa gca gca gca act tgt gat ata aaa ttt att tct tta gat 672
 Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp
 210 215 220

gat gat ctc ata gat aaa tta cat act aag tat ccc tat tat aaa agg 720
 Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg
 225 230 235 240

gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act 768
 Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr
 245 250 255

gtt tca gta aaa gct tct tta ata aca act act gaa tta agc aat gag 816
 Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu
 260 265 270

ttg gcc tat aaa gtt gtt aaa tct ttg gtt agc cat tta cat gaa cta 864
 Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu
 275 280 285

cat gga att act gga gct ctt aga aat ctt act gta aaa gac atg gta 912
 His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val
 290 295 300

cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag 960
 Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys
 305 310 315 320

gaa att gga gtt ata aaa taa 981
 Glu Ile Gly Val Ile Lys
 325

<210> 7
 <211> 326
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <400> 7

Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys
 1 5 10 15

Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile
 20 25 30

Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly
 35 40 45

Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser
 50 55 60

Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu
275 280 285

His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val
290 295 300

Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys
305 310 315 320

Glu Ile Gly Val Ile Lys
325

<210> 8

<211> 756

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

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<222> (1)..(756)

<223> Corresponds to SEQ ID NO:2, nucleotides 2611..3366

Hypothetical o-sialoglycoprotein endopeptidase

Product="lhworf4"

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atg atg gct aaa gct att tcc agc gtt act aat aag cct att att gag 48
Met Met Ala Lys Ala Ile Ser Ser Val Thr Asn Lys Pro Ile Ile Glu
1 5 10 15

gtt aat cat ctg gaa gca cat act ttg cta ata cga atg ttt cat gat 96
Val Asn His Leu Glu Ala His Thr Leu Leu Ile Arg Met Phe His Asp
20 25 30

att gat ttt cca ttt tta gta ttg atc ata tct ggc gga cat tgt cag 144
Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln
35 40 45

ttt tta ata gtt cat gat gtt gga tgt tat caa aga tta ggt tct tct 192
Phe Leu Ile Val His Asp Val Gly Cys Tyr Gln Arg Leu Gly Ser Ser
50 55 60

tta gat gac tcc ctt ggt gaa gta ttt gat aaa gta gca aga atg ttg 240
Leu Asp Asp Ser Leu Gly Glu Val Phe Asp Lys Val Ala Arg Met Leu
65 70 75 80

aat ttg gga tat cct gga ggg cca att att gaa aaa aaa tcc ata atg 288
Asn Leu Gly Tyr Pro Gly Gly Pro Ile Ile Glu Lys Lys Ser Ile Met
85 90 95

ggt gat agc aaa agt ttt ttt cta cca cgt gca tta atc aat cgt ctt 336
Gly Asp Ser Lys Ser Phe Phe Leu Pro Arg Ala Leu Ile Asn Arg Leu
100 105 110

gga tgt gat ttt tct ttc tcc ggt att aag acg gca gta aga aat att 384
 Gly Cys Asp Phe Ser Phe Ser Gly Ile Lys Thr Ala Val Arg Asn Ile
 115 120 125

gtt gta aat caa aaa tat ata gat aat gat ttt ata tgt aat att tca 432
 Val Val Asn Gln Lys Tyr Ile Asp Asn Asp Phe Ile Cys Asn Ile Ser
 130 135 140

gct tct ttt caa gat tgt att ggt gat ata tta gta aac agg att act 480
 Ala Ser Phe Gln Asp Cys Ile Gly Asp Ile Leu Val Asn Arg Ile Thr
 145 150 155 160

aat gct att cat atg tca caa gct ata aat tgt aag att aat aag tta 528
 Asn Ala Ile His Met Ser Gln Ala Ile Asn Cys Lys Ile Asn Lys Leu
 165 170 175

gta gta act gga ggt gtt gca gct aat cac cta tta cgt aat cgt ata 576
 Val Val Thr Gly Gly Val Ala Ala Asn His Leu Leu Arg Asn Arg Ile
 180 185 190

tca att tgt gta aaa gat aat aat ttt gag gtg cta tat cct cca act 624
 Ser Ile Cys Val Lys Asp Asn Asn Phe Glu Val Leu Tyr Pro Pro Thr
 195 200 205

gag tta tgt act gat aat gga att atg gtt ggg tgg gct ggt att gaa 672
 Glu Leu Cys Thr Asp Asn Gly Ile Met Val Gly Trp Ala Gly Ile Glu
 210 215 220

aat tta tct aaa ggt tat gtt tct aat tta gat ttt gtt cca aaa gca 720
 Asn Leu Ser Lys Gly Tyr Val Ser Asn Leu Asp Phe Val Pro Lys Ala
 225 230 235 240

aga tgg ccg tta gaa agc ata aaa agg tct agt taa 756
 Arg Trp Pro Leu Glu Ser Ile Lys Arg Ser Ser
 245 250

<210> 9

<211> 251

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 9

Met Met Ala Lys Ala Ile Ser Ser Val Thr Asn Lys Pro Ile Ile Glu
 1 5 10 15

Val Asn His Leu Glu Ala His Thr Leu Leu Ile Arg Met Phe His Asp
 20 25 30

Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln
 35 40 45

<211> 222
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

 <220>
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 <223> Corresponds to SEQ ID NO:2, nucleotides 4065..4286
 Product="lhworf5"

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 1 5 10 15

 aaa aat ttt tta att tat atg aca ttt gta tat tac tat aaa tca gta 96
 Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Tyr Lys Ser Val
 20 25 30

 ttt att aaa gtt aag aat att aat aat gta ttt aag ttt aaa aaa aac 144
 Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn
 35 40 45

 ttt ttt gta aat agt cat att aat ata act ttt agc aat ata aat att 192
 Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile
 50 55 60

 gaa ttt tca gta ctt acg tca tac tgt taa 222
 Glu Phe Ser Val Leu Thr Ser Tyr Cys
 65 70

<210> 11
 <211> 73
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 11

 Met Thr Leu Phe Tyr Tyr Arg Lys Phe Thr Asn Leu Thr Ile Val Asn
 1 5 10 15

 Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Tyr Lys Ser Val
 20 25 30

 Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn
 35 40 45

 Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile
 50 55 60

Glu Phe Ser Val Leu Thr Ser Tyr Cys
65 70

<210> 12
<211> 4913
<212> DNA
<213> *Ehrlichia ruminantium* (formerly *Cowdria ruminantium*)

<400> 12
gatcttatta tatgaacatc ctaataatta acattaaaat taatgtgtta ttagaaagca 60
tgtctaagaa aatatatctt ataaatttac agtcaagatt gcattgacta agtattttta 120
atatagattt gtagtaacta ctatgtaaag tgcattttat ataattttta ataaataaat 180
aaaaaaggta agattatgaa tatattcaat tatatgcaga taatgcctaa tataagtgtt 240
gatgcatttg ttgcacctac tgctgtaatt ataggtgatg tttgtgtaaa tgacaagtgt 300
agcatttggt ataactcagt attacgtgga gatgtaggcc aaattgttat tgggtgtaggt 360
actaatattc aagatgggac aataatacat gttgatagga aatatggtaa tacgaatatt 420
ggcaaaaagg ttactattgg gcattgggtg atattacatg cttgtgagat acaagattat 480
gtgcttggtg gaatgggac tattattatg gataacgttg tgggtgaaaa gaatgcaatg 540
gtggctgctg gatcattagt ggtaagaggt aaagttgtga aaactgggta attatgggct 600
ggtaggcctg cacaattttt aagaatgttg tctagtgatg aaattaaaga gataagtaaa 660
tctgctgata actatataga gcttgccagt gattacataa ctggtaagtt gtaatttttag 720
ttacgctcaa aagataatta tctgtattga ttgagaattt actagtgttt ttttatttta 780
tatgaatcta tgctatggat gactctatat tctatgtttc aattaattac tagatgtagc 840
ctaggaagta gggttttgta ttatttcatt attattgttt taaactatgt tagtaatatc 900
tgtaaaatgg gtagattact tatgtagtat agattttaat taacaattaa agttaaatc 960
ctttaatgtg tgtaattct ggtgaatact tttattcaag tattttaatt acttagtata 1020
ttcttgatgg tgtgggttgt tgaaaattac ttttctgtta taggatggag aataaattca 1080
tgtagttat gattggtgaa attagtgatg tataaattat aaatcaaagtg tgctaatttg 1140
ttgacaatgg gaatttctat gatttatgct atggattata catcatatga tggtgggttt 1200
gtatgtaatt tatagtaaat aagtagtttt ttttattata tttcatatgt cattttttgt 1260
gttgagtgtg gtctaaggaa tttttgtgg tgcatttatg agtgaagtac aagtaagggc 1320

tgaaaatctt ggtggtgagt caatattaga agctccaatt cgagtttctg ttaagattgg 1380
 tgatagtatt aagcaagggtg atgtattggt tatcattgaa acggataaaa cttctctaga 1440
 aattgtatct cctgtagatg gaacagttag taaagtattt atagcagatg aagaaattat 1500
 agaacgtgat caacttttat gtacaataaa tgttggtgaa ttatcacata ttgtccagtc 1560
 tcaaactcag gatcctaaaa cagataatgg tgatattatt aatgatgata ttcagacggt 1620
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 gaatcagatc aatgggtctg gtattggtgg aagaattaca aaatctgatg ttttagacca 1740
 cattaatggt gtttcaaaag atcatagtgt gctttctgaa caatgtagta ttacttctca 1800
 tgagaagaga gaagaacgtg ttaagatgag taaaattagg cagggtgattg ctgcgaggct 1860
 taaggagtct caaaatactg ctgcaatatt aactacgttt aatgaagtgg atatgaagaa 1920
 tgttatggat cttcgtgttc agtataggga gacctttgaa aagaaatatg gtgtcaaaact 1980
 tggatttatg tcttttttta taaaagcggg agtattagca ttaaaagaat taccagtaat 2040
 taatgctgag atatctggta atgagattat atataaacat tattatgaca taggtattgc 2100
 tgtagggaca gacaaagggtc tagttgttcc agtaatgctg gatgctgata agatgtcttg 2160
 tgctgagctt gagttaacct tagcttcttt aggtaagaaa gctaggggaag ggaaattaga 2220
 agtttcagat atggctgggtg caacttttac tattactaat ggtgggggtat atggttcatt 2280
 attatctact cctataatta atcctcctca gtctggtatt ttaggtatgc actctataca 2340
 aaaacgacca gtagtagtta atgataattc tatagagatt agacctatga tgtacattgc 2400
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 taaacagtat attgaagatc caagtagaat gtttctagaa atataaatta tgtatatcgg 2520
 catttcacaa tcatagcagt aattgtttaa catcttgagt ttctgtatat tttacgaagt 2580
 aatgtacaag gttgctgtct gacaatatta agtttttagtg ggttttgttt attggtttat 2640
 tgттаagtaa ttatagtaaa gtataataaa tgtaatacag ttatagtgtc gatatagcta 2700
 atagtgcagg gaatattagt gtttacgcat atataataat agaaattgta tataattctt 2760
 agtgттаatt attttatggt gttatataaa aacgatctca aaaagtatta atttatataa 2820
 aaataaaaac taaatttttag atggctttat tgcaatgtct tttatgttgt tatatgagtt 2880
 aatgtttaat taaaaagtta tgttatagta taaaaataaa tgtaacattt ctttagctat 2940
 gcgaaatata taaaactttc tttatcactg tgatgttttt gtagagctat ctatgaacat 3000

attgaaatgt taacattatt gaatgttttt cttgtaatta tacgttaatg tataggttat 3060
 ttggtaaaag gtagagcta aatcttgtgt taatataaaa aattaaattg tacggtaatg 3120
 taaattttatt aagctacatc ttttctgtaa aaaatttttg tatttctgtc atctgatgta 3180
 taaggttaca aatgcagaaa tgtaaagtag tttatatgta tgaaggctat ggtagcctat 3240
 ataagattgc ctacacatat tataattatc tattgatact tttagtagta ctaatatgat 3300
 aagaatatga ctaaattttt ttattgcata taaaaagtag cagtagttgt ttagagtaa 3360
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 ttaagaaatt aaagaatcaa aatttaaagt tattatatct taattatcta aattttgttg 3480
 ataggtaatc ctattttttg aataagaagt gtgtagttta tgattaacaa aacattgttg 3540
 atgtatttcg taatagtata ttaacagaat ttttgtatgt ttatttttta gaatttaata 3600
 aaaaatttta tatattttaa aaaaaatta acatcttatt gtatttgtat tacactggtt 3660
 ataagggtgtg ttagcgggtg tttgtatggt gttgagtaaa gataaaaata aaaagaaaaa 3720
 agatcccaat aatcaagaaa atgatgaaag gaatcaaact ggtgaatcag gtgttaaacc 3780
 tgaagtacca aaccagcaaa gtattcaaga tataggtcag ggtgtagtag aaggggcaac 3840
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 gatgttatca aatatcacta aacattctga cgaggtgtt gttcttgtga agttaaatct 4560
 tatgtcacia tatttgcttg catttggtgc gtatcaggta agccggtcaa tgtaaacaca 4620

gaagcttagt aattctgatt tttatgcaat tgatattttg ttattagaat taatattggt 4680
 ttcgtacaag gagagagtga atctttattg tgctcaaaga gaagttctta ggatgtatgc 4740
 tataatggat tataattctg gttataatcc taattgtagt aatataaagt tttgttatgt 4800
 aatggtgcaa ttattccgtg atttattatc tgcaagacaa agtatggtgt taggtgattt 4860
 agatttaciaa ttagttaatt tattgattat cagtgttagt attcaaatag atc 4913

<210> 13
 <211> 519
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(519)
 <223> Corresponds to SEQ ID NO:12, nucleotides 196..714
 Hypothetical ferripyochelin binding protein
 Product="4hworf1"

<400> 13
 atg aat ata ttc aat tat atg cag ata atg cct aat ata agt gtt gat 48
 Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
 1 5 10 15
 gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat 96
 Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
 20 25 30
 gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc 144
 Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
 35 40 45
 caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata 192
 Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
 50 55 60
 cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act 240
 His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65 70 75 80
 att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg 288
 Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
 85 90 95
 ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag 336
 Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
 100 105 110
 aat gca atg gtg gct gct gga tca tta gtg gta aga ggt aaa gtt gtg 384
 Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val

115	120	125	
aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg			432
Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met			
130	135	140	
ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat			480
Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr			
145	150	155	160
ata gag ctt gcc agt gat tac ata act ggt aag ttg taa			519
Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu			
165	170		

<210> 14
 <211> 172
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 14

Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp	
1	15

Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn	
20	30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly	
35	45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile	
50	60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr	
65	80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val	
85	95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys	
100	110

Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val	
115	125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met

130

135

140

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
 145 150 155 160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
 165 170

<210> 15

<211> 1209

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(1209)

<223> Corresponds to SEQ ID NO:12, nucleotides 1298..2506
 Hypothetical dihydrolipoamide acetyltransferase
 Product="4hworf2"

<400> 15

atg agt gaa gta caa gta agg gct gaa aat ctt ggt ggt gag tca ata 48
 Met Ser Glu Val Gln Val Arg Ala Glu Asn Leu Gly Gly Glu Ser Ile
 1 5 10 15

tta gaa gct cca att cga gtt tct gtt aag att ggt gat agt att aag 96
 Leu Glu Ala Pro Ile Arg Val Ser Val Lys Ile Gly Asp Ser Ile Lys
 20 25 30

caa ggt gat gta ttg ttt atc att gaa acg gat aaa act tct cta gaa 144
 Gln Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu
 35 40 45

att gta tct cct gta gat gga aca gtt agt aaa gta ttt ata gca gat 192
 Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp
 50 55 60

gaa gaa att ata gaa cgt gat caa ctt tta tgt aca ata aat gtt ggt 240
 Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly
 65 70 75 80

gaa tta tca cat att gtc cag tct caa act cag gat cct aaa aca gat 288
 Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp
 85 90 95

aat ggt gat att att aat gat gat att cag acg ttt ata cag aaa aaa 336
 Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys
 100 105 110

gat gct cct tct gca gta aaa att atg gca gaa aat tca att gat aag 384
 Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys

115	120	125	
aat cag atc aat ggg tct ggt att ggt gga aga att aca aaa tct gat			432
Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp			
130	135	140	
ggt tta gac cac att aat gtt gtt tca aaa gat cat agt gtg ctt tct			480
Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser			
145	150	155	160
gaa caa tgt agt att act tct cat gag aag aga gaa gaa cgt gtt aag			528
Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys			
165	170	175	
atg agt aaa att agg cag gtg att gct gcg agg ctt aag gag tct caa			576
Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln			
180	185	190	
aat act gct gca ata tta act acg ttt aat gaa gtg gat atg aag aat			624
Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn			
195	200	205	
ggt atg gat ctt cgt gtt cag tat agg gag acc ttt gaa aag aaa tat			672
Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr			
210	215	220	
ggt gtc aaa ctt gga ttt atg tct ttt ttt ata aaa gcg gta gta tta			720
Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu			
225	230	235	240
gca tta aaa gaa tta cca gta att aat gct gag ata tct ggt aat gag			768
Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu			
245	250	255	
att ata tat aaa cat tat tat gac ata ggt att gct gta ggg aca gac			816
Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp			
260	265	270	
aaa ggt cta gtt gtt cca gta atg cgt gat gct gat aag atg tct tgt			864
Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys			
275	280	285	
gct gag ctt gag tta acc tta gct tct tta ggt aag aaa gct agg gaa			912
Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu			
290	295	300	
ggg aaa tta gaa gtt tca gat atg gct ggt gca act ttt act att act			960
Gly Lys Leu Glu Val Ser Asp Met Ala Gly Ala Thr Phe Thr Ile Thr			
305	310	315	320
aat ggt ggg gta tat ggt tca tta tta tct act cct ata att aat cct			1008
Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro			
325	330	335	
cct cag tct ggt att tta ggt atg cac tct ata caa aaa cga cca gta			1056

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val
 340 345 350

gta gtt aat gat aat tct ata gag att aga cct atg atg tac att gca 1104
 Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala
 355 360 365

tta tct tat gat cat aga att gtt gat gga caa ggt gct gta aca ttt 1152
 Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe
 370 375 380

tta gta aga gtt aaa cag tat att gaa gat cca agt aga atg ttt cta 1200
 Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu
 385 390 395 400

gaa ata taa 1209
 Glu Ile

<210> 16
 <211> 402
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 16

Met Ser Glu Val Gln Val Arg Ala Glu Asn Leu Gly Gly Glu Ser Ile
 1 5 10 15

Leu Glu Ala Pro Ile Arg Val Ser Val Lys Ile Gly Asp Ser Ile Lys
 20 25 30

Gln Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu
 35 40 45

Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp
 50 55 60

Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly
 65 70 75 80

Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp
 85 90 95

Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys
 100 105 110

Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys
115 120 125

Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp
130 135 140

Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser
145 150 155 160

Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys
165 170 175

Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln
180 185 190

Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn
195 200 205

Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr
210 215 220

Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu
225 230 235 240

Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu
245 250 255

Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp
260 265 270

Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys
275 280 285

Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu
290 295 300

Gly Lys Leu Glu Val Ser Asp Met Ala Gly Ala Thr Phe Thr Ile Thr
305 310 315 320

Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro
325 330 335

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val
340 345 350

Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala
355 360 365

Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe
370 375 380

Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu
385 390 395 400

Glu Ile

<210> 17
<211> 1227
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(1227)
<223> Corresponds to SEQ ID NO:12, nucleotides 3686...>4913
Product="4hworf3i"

<400> 17
atg ttg ttg agt aaa gat aaa aat aaa aag aaa aaa gat ccc aat aat 48
Met Leu Leu Ser Lys Asp Lys Asn Lys Lys Lys Lys Asp Pro Asn Asn
1 5 10 15

caa gaa aat gat gaa agg aat caa act ggt gaa tca ggt gtt aaa cct 96
Gln Glu Asn Asp Glu Arg Asn Gln Thr Gly Glu Ser Gly Val Lys Pro
20 25 30

gaa gta cca aac cag caa agt att caa gat ata ggt cag ggt gta gta 144
Glu Val Pro Asn Gln Gln Ser Ile Gln Asp Ile Gly Gln Gly Val Val
35 40 45

gaa ggg gca aca gat gct agt gat atg agt ggt gtt gga aga tgt gct 192
Glu Gly Ala Thr Asp Ala Ser Asp Met Ser Gly Val Gly Arg Cys Ala
50 55 60

ttt tct gtg act ata gag att gaa tca tct tca tca aca tct cag cca 240
Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro
65 70 75 80

agt agt agt ctt gaa aat ata tat atg agg cag ggt gct agg cca aaa 288

Ser Ser Ser Leu Glu Asn Ile Tyr Met Arg Gln Gly Ala Arg Pro Lys
 85 90 95
 act agg act caa agt aaa gtt gca cag cag agt aca gga caa ttt cag 336
 Thr Arg Thr Gln Ser Lys Val Ala Gln Gln Ser Thr Gly Gln Phe Gln
 100 105 110
 agt ata ggg tca cag agt agt ttg cct cct gta ttt gta aaa cgt atg 384
 Ser Ile Gly Ser Gln Ser Ser Leu Pro Pro Val Phe Val Lys Arg Met
 115 120 125
 gct gat gta tct ttg gaa aag gca gaa tgt gat aca tat ata tgt ggg 432
 Ala Asp Val Ser Leu Glu Lys Ala Glu Cys Asp Thr Tyr Ile Cys Gly
 130 135 140
 act aaa agg cgt agc gat caa agc aca agg tca agg gag gac tta cct 480
 Thr Lys Arg Arg Ser Asp Gln Ser Thr Arg Ser Arg Glu Asp Leu Pro
 145 150 155 160
 tct agg ttt gca aaa tgt gca tct gat ata ttt tta aca aag cca caa 528
 Ser Arg Phe Ala Lys Cys Ala Ser Asp Ile Phe Leu Thr Lys Pro Gln
 165 170 175
 aat aat gat cta gat att cat gat act gat aaa gag aaa tta ata cat 576
 Asn Asn Asp Leu Asp Ile His Asp Thr Asp Lys Glu Lys Leu Ile His
 180 185 190
 tca tta gaa gaa tta gat gtt gct ctg cct act gag tct gga ggt gat 624
 Ser Leu Glu Glu Leu Asp Val Ala Leu Pro Thr Glu Ser Gly Gly Asp
 195 200 205
 cat aat gtt tta tct gat gtc gta tat aaa aaa tgt gta tcc tta caa 672
 His Asn Val Leu Ser Asp Val Val Tyr Lys Lys Cys Val Ser Leu Gln
 210 215 220
 caa aaa tgt ggc agt ttt aga cag ttt agt aat tct tgt cta gca aga 720
 Gln Lys Cys Gly Ser Phe Arg Gln Phe Ser Asn Ser Cys Leu Ala Arg
 225 230 235 240
 tta aga ggt atg cat atg gga tat ctt aat ttt ttt atg aaa cga ttg 768
 Leu Arg Gly Met His Met Gly Tyr Leu Asn Phe Phe Met Lys Arg Leu
 245 250 255
 ttt atg gct caa ggt aac aca tta gtt atg cgt ggg gag tac ttg cag 816
 Phe Met Ala Gln Gly Asn Thr Leu Val Met Arg Gly Glu Tyr Leu Gln
 260 265 270
 atg tta tca aat atc act aaa cat tct gac gag gct gtt gtt ctt gtg 864
 Met Leu Ser Asn Ile Thr Lys His Ser Asp Glu Ala Val Val Leu Val
 275 280 285
 aag tta aat ctt atg tca caa tat ttg ctt gca ttt ggt gcg tat cag 912
 Lys Leu Asn Leu Met Ser Gln Tyr Leu Leu Ala Phe Gly Ala Tyr Gln
 290 295 300

gta agc cgg tca atg tta aca cag aag ctt agt aat tct gat ttt tat 960
 Val Ser Arg Ser Met Leu Thr Gln Lys Leu Ser Asn Ser Asp Phe Tyr
 305 310 315 320

gca att gat att ttg tta tta gaa tta ata ttg gtt tcg tac aag gag 1008
 Ala Ile Asp Ile Leu Leu Leu Glu Leu Ile Leu Val Ser Tyr Lys Glu
 325 330 335

aga gtg aat ctt tat tgt gct caa aga gaa gtt ctt agg atg tat gct 1056
 Arg Val Asn Leu Tyr Cys Ala Gln Arg Glu Val Leu Arg Met Tyr Ala
 340 345 350

ata atg gat tat aat tct ggt tat aat cct aat tgt agt aat ata aag 1104
 Ile Met Asp Tyr Asn Ser Gly Tyr Asn Pro Asn Cys Ser Asn Ile Lys
 355 360 365

ttt tgt tat gta atg gtg caa tta ttc cgt gat tta tta tct gca aga 1152
 Phe Cys Tyr Val Met Val Gln Leu Phe Arg Asp Leu Leu Ser Ala Arg
 370 375 380

caa agt atg gtg tta ggt gat tta gat tta caa tta gtt aat tta ttg 1200
 Gln Ser Met Val Leu Gly Asp Leu Asp Leu Gln Leu Val Asn Leu Leu
 385 390 395 400

att atc agt gtt agt att caa ata gat 1227
 Ile Ile Ser Val Ser Ile Gln Ile Asp
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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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 1 5 10 15

Gln Glu Asn Asp Glu Arg Asn Gln Thr Gly Glu Ser Gly Val Lys Pro
 20 25 30

Glu Val Pro Asn Gln Gln Ser Ile Gln Asp Ile Gly Gln Gly Val Val
 35 40 45

Glu Gly Ala Thr Asp Ala Ser Asp Met Ser Gly Val Gly Arg Cys Ala
 50 55 60

Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro
 65 70 75 80

Ser Ser Ser Leu Glu Asn Ile Tyr Met Arg Gln Gly Ala Arg Pro Lys
85 90 95

Thr Arg Thr Gln Ser Lys Val Ala Gln Gln Ser Thr Gly Gln Phe Gln
100 105 110

Ser Ile Gly Ser Gln Ser Ser Leu Pro Pro Val Phe Val Lys Arg Met
115 120 125

Ala Asp Val Ser Leu Glu Lys Ala Glu Cys Asp Thr Tyr Ile Cys Gly
130 135 140

Thr Lys Arg Arg Ser Asp Gln Ser Thr Arg Ser Arg Glu Asp Leu Pro
145 150 155 160

Ser Arg Phe Ala Lys Cys Ala Ser Asp Ile Phe Leu Thr Lys Pro Gln
165 170 175

Asn Asn Asp Leu Asp Ile His Asp Thr Asp Lys Glu Lys Leu Ile His
180 185 190

Ser Leu Glu Glu Leu Asp Val Ala Leu Pro Thr Glu Ser Gly Gly Asp
195 200 205

His Asn Val Leu Ser Asp Val Val Tyr Lys Lys Cys Val Ser Leu Gln
210 215 220

Gln Lys Cys Gly Ser Phe Arg Gln Phe Ser Asn Ser Cys Leu Ala Arg
225 230 235 240

Leu Arg Gly Met His Met Gly Tyr Leu Asn Phe Phe Met Lys Arg Leu
245 250 255

Phe Met Ala Gln Gly Asn Thr Leu Val Met Arg Gly Glu Tyr Leu Gln
260 265 270

Met Leu Ser Asn Ile Thr Lys His Ser Asp Glu Ala Val Val Leu Val
275 280 285

Lys Leu Asn Leu Met Ser Gln Tyr Leu Leu Ala Phe Gly Ala Tyr Gln
290 295 300

Val Ser Arg Ser Met Leu Thr Gln Lys Leu Ser Asn Ser Asp Phe Tyr
305 310 315 320

Ala Ile Asp Ile Leu Leu Leu Glu Leu Ile Leu Val Ser Tyr Lys Glu
325 330 335

Arg Val Asn Leu Tyr Cys Ala Gln Arg Glu Val Leu Arg Met Tyr Ala
340 345 350

Ile Met Asp Tyr Asn Ser Gly Tyr Asn Pro Asn Cys Ser Asn Ile Lys
355 360 365

Phe Cys Tyr Val Met Val Gln Leu Phe Arg Asp Leu Leu Ser Ala Arg
370 375 380

Gln Ser Met Val Leu Gly Asp Leu Asp Leu Gln Leu Val Asn Leu Leu
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Ile Ile Ser Val Ser Ile Gln Ile Asp
405

<210> 19

<211> 6190

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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aagtttttat ttacaaaaga cttgctataa atcgcaatac aaaatattga atacatgaac	180
aaaattgaag aaccaaacat taattgataa agtatattgt tattatatac ctacaactat	240
tatttgtatc atatgacaat ttcttattaa ataatagtaa aaataatttt tatacagcaa	300
gatttgatac ttaccataat aaagtatcac aacaaaacca tataaaataa gaaagtagta	360
cacacattat aaaaataacg ttaatcacc attgcaatga cataataagt tacatgggta	420
cacttttgat acttataata gttaataata aaagtagtat aataaaacca aaaccatata	480
aaataagaaa gtaccacaca ttatagaaat aataccgggc acccattgca atgacataat	540
aagttacatg ggtacacttt tgacacttat aatagttaat aataaaagta gtataacaaa	600

actaaaacca tataaaataa gaaagtacca cacattacag aaacaatact ggtcacacat	660
tgcaatgaca taataagtta catgggtaca cttttgatac ttataatagt taataataaa	720
agtagtataa taaaacccaaa accatataaa ataagaaagt accacacatt acagaaacaa	780
tactgggtcac ccattgcaat gacataataa gttacatggg tacacttttg atacttataa	840
tagttaataa taaaagtagt ataataaaac caaaaccata taaaataaga aagtaccaca	900
cattacagaa ataataccgg tcacccattg caatagcata ataagttata ttaatacacg	960
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acgttccttc agtagcagca cgtgtatact ctgttactct attttcaaag aaattagtgt	1920
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taggctctaa atttaactgt attagccttc tatttgcaat atatcttata tattctttta	2040
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tcttcagatc 6190

<210> 20
<211> 975
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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<222> (1)..(975)
<223> Complement to SEQ ID NO:19, nucleotides 1835..2809
Hypothetical ribonucleoside reductase, beta chain
Product="6hworf1"

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ctaagatct tcaaagcgtt cttccacgt tcttcagta gcagcacgtg tataactctgt 60
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caaagggttc ttatttgctc tgtatatagg ctctaaattt aactgtatta gccttctatt 180
tgcaatatat cttatatatt ctttaacctc ctgagcagac aaaccttcaa catcaccaca 240
agcaaagtc aaattaataa actcatcttc taaagttaca ataactactac atgcttcata 300
caattccttt ttaagatcat catcccatat ttcataattt tcttgaataa aagtattaaa 360
taatctaatt atcgactcag tatgtaatgt ttcatcacga acagaccaag caataatttg 420
tcccatgcct ttcattttcc caaacggtg aaaatttagt aaaattgcaa atgaagcaaa 480

caattgtaaa ccttctgtaa aggcaccaaaa aactgctaaa gtttttgcta catgcctttt 540
 gtcattcttt ctacactctt caaacggttg catgtagtca tatttctttt tcataacctc 600
 aaatttcaaa aacgcctgat actctatttc tggcatccca atagtatcca ataagtaaga 660
 ataagcagca atatgtatag tttccatatt tgaaaaatgca gataacatca tacatatttc 720
 cgttggctta aatatatttg aataatgttt catataacag ttattaactt cgatatcagc 780
 ctgtgtaaaa aaacgaaaaa tttgtactaa aaggttcttt tccttatcag aaagtacagt 840
 cttccaatct tgaacatcat ctgcaagagg cacttcttca ggcaaccagt gtatcctctg 900
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 atctagtaat gacat 975

<210> 21
 <211> 1947
 <212> DNA
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 <221> CDS
 <222> (1)..(1947)
 <223> Corresponds to SEQ ID NO:19, nucleotides 3126..5072
 Product = "6hworf2"

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 1 5 10 15
 ata ttt gca gac tct cag att cac ata aca gag gaa caa tta aaa ata 96
 Ile Phe Ala Asp Ser Gln Ile His Ile Thr Glu Glu Gln Leu Lys Ile
 20 25 30
 tat ata aag aat ctt ata gat aac tta tat gta tat aac cta cta gat 144
 Tyr Ile Lys Asn Leu Ile Asp Asn Leu Tyr Val Tyr Asn Leu Leu Asp
 35 40 45
 cct gga aat gct ata cca ttg tct att ata gca atg cta ggt cta cat 192
 Pro Gly Asn Ala Ile Pro Leu Ser Ile Ile Ala Met Leu Gly Leu His
 50 55 60
 tca gat ttt cat tca ttt aaa aaa gca gta cta gat act ctt tct gga 240
 Ser Asp Phe His Ser Phe Lys Lys Ala Val Leu Asp Thr Leu Ser Gly
 65 70 75 80
 tac aaa aat tct gtc cat agt ttt ctt gca cag tct aca ata att gac 288
 Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp
 85 90 95

agg tct gaa tct tta aga gca gaa cca aat cac tgc tta tat tca tta 336
 Arg Ser Glu Ser Leu Arg Ala Glu Pro Asn His Cys Leu Tyr Ser Leu
 100 105 110

cca cct ctt ttg gat aaa aga act tca gaa gat atg tgg aat gat att 384
 Pro Pro Leu Leu Asp Lys Arg Thr Ser Glu Asp Met Trp Asn Asp Ile
 115 120 125

aaa gaa tta cac ata tta tat cac caa tat ata att aac gta tct gta 432
 Lys Glu Leu His Ile Leu Tyr His Gln Tyr Ile Ile Asn Val Ser Val
 130 135 140

gat aaa agt act aat gct ata agc aat aca gta aat gct cca ggc acc 480
 Asp Lys Ser Thr Asn Ala Ile Ser Asn Thr Val Asn Ala Pro Gly Thr
 145 150 155 160

aaa aca tgt tct att aag ata tcg tat act aat cca tta aga cag cat 528
 Lys Thr Cys Ser Ile Lys Ile Ser Tyr Thr Asn Pro Leu Arg Gln His
 165 170 175

gta cac tat ttt aca tta aaa aca ctt att gaa tat tac aac act caa 576
 Val His Tyr Phe Thr Leu Lys Thr Leu Ile Glu Tyr Tyr Asn Thr Gln
 180 185 190

caa aca tca tta aca ggt cac aga tca att gat gat caa caa gaa gct 624
 Gln Thr Ser Leu Thr Gly His Arg Ser Ile Asp Asp Gln Gln Glu Ala
 195 200 205

gct gtt act ttg ttt aaa gaa aca tta gaa gaa aaa ttt tgc aaa gga 672
 Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly
 210 215 220

tta aaa aat aaa ata ttt ttt aat tat gca caa tat tta aaa agt cta 720
 Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu
 225 230 235 240

ttt act atc gta aca tca aat cca aaa gta gac tat acc ctt cca caa 768
 Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln
 245 250 255

aat ata tat aga tat tgt gaa aca aga aga atg gta att tca aaa ata 816
 Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile
 260 265 270

aca cat gat ata att cct ata tca gat cca gga act gat ata cgt att 864
 Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile
 275 280 285

tat tgt gat ata cca gag tat gta acc gta tta tca gaa aca agt aac 912
 Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn
 290 295 300

att act ata tac ggg aaa gaa gta ctt ggt aaa gtt tat agc ata tat 960
 Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr

305	310	315	320	
ggt aca att ata att aaa aac aat atg cca cat aat gaa cga gaa ata				1008
Gly Thr Ile Ile Ile Lys Asn Asn Met Pro His Asn Glu Arg Glu Ile				
	325	330	335	
agc tct cgt ata tgt tct tta ttt ggt cgt gtt ata atc aat gga aga				1056
Ser Ser Arg Ile Cys Ser Leu Phe Gly Arg Val Ile Ile Asn Gly Arg				
	340	345	350	
ata ctt aat cgg aaa cat aca ata cct agt ata ttt gaa att aac aac				1104
Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn				
	355	360	365	
cat aac aca tac tta tca ctt aaa tat aat tct ata tta aca aaa ata				1152
His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile				
	370	375	380	
aca agc agc tct gta ggt tcc gta aat gaa gaa aaa aaa tca caa atc				1200
Thr Ser Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile				
	385	390	400	
ttt gaa atc agt agg gat aca att ttg aat tca aca aat tat cag aga				1248
Phe Glu Ile Ser Arg Asp Thr Ile Leu Asn Ser Thr Asn Tyr Gln Arg				
	405	410	415	
aat ata tca aat tta aaa ata gaa cta cat aac cca gat gaa caa ctc				1296
Asn Ile Ser Asn Leu Lys Ile Glu Leu His Asn Pro Asp Glu Gln Leu				
	420	425	430	
aca gct act gtc ata tca tta gat tta aaa gat cat cca tta cct att				1344
Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile				
	435	440	445	
act aat aat aat act ata cct aat ata tta agc cta aca gac aat cac				1392
Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His				
	450	455	460	
gca aca gat tca gaa tta cca agt gag ttt ttt agt aac aat gtt aac				1440
Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn				
	465	470	480	
cca aaa agt gct gga att acg aga ata aaa aat aca att att att gag				1488
Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Ile Glu				
	485	490	495	
aaa tta act cct aca ata gga aga tat atg aat gtt gcc aca aaa aat				1536
Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn				
	500	505	510	
gga aca gta tta gat aaa tat ggg atc aca gaa gta att att caa agt				1584
Gly Thr Val Leu Asp Lys Tyr Gly Ile Thr Glu Val Ile Ile Gln Ser				
	515	520	525	
acc aga aac ttt gta ata tta tta cta cat gat gca aat gtt act ata				1632

Thr Arg Asn Phe Val Ile Leu Leu Leu His Asp Ala Asn Val Thr Ile
 530 535 540

gaa tgt cca ttt tct gga gaa ata ttt aca aat aca ggt aat att aca 1680
 Glu Cys Pro Phe Ser Gly Glu Ile Phe Thr Asn Thr Gly Asn Ile Thr
 545 550 555 560

gtt att ggc cca gta act cac aat tct aaa ctt att tca aac ttt ggt 1728
 Val Ile Gly Pro Val Thr His Asn Ser Lys Leu Ile Ser Asn Phe Gly
 565 570 575

tca gtt tat gtt ggt aat ata tct cat cgg tca aat gca tta gca ata 1776
 Ser Val Tyr Val Gly Asn Ile Ser His Arg Ser Asn Ala Leu Ala Ile
 580 585 590

gat aac agc cgt att gta tct tca ctt ggg cat gtc aca att tat ggc 1824
 Asp Asn Ser Arg Ile Val Ser Ser Leu Gly His Val Thr Ile Tyr Gly
 595 600 605

aaa gtt agt aaa tcc aat att act act tct aca tca gat gca ata tca 1872
 Lys Val Ser Lys Ser Asn Ile Thr Thr Ser Thr Ser Asp Ala Ile Ser
 610 615 620

ata cat aac tca ata tca tgg ttt gat aaa cta act tct tgt aac acc 1920
 Ile His Asn Ser Ile Ser Trp Phe Asp Lys Leu Thr Ser Cys Asn Thr
 625 630 635 640

aaa act tta gca tct cgc aaa aca taa 1947
 Lys Thr Leu Ala Ser Arg Lys Thr
 645

<210> 22
 <211> 648
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <400> 22

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Ile Phe Ala Asp Ser Gln Ile His Ile Thr Glu Glu Gln Leu Lys Ile
 20 25 30

Tyr Ile Lys Asn Leu Ile Asp Asn Leu Tyr Val Tyr Asn Leu Leu Asp
 35 40 45

Pro Gly Asn Ala Ile Pro Leu Ser Ile Ile Ala Met Leu Gly Leu His
 50 55 60

Ser Asp Phe His Ser Phe Lys Lys Ala Val Leu Asp Thr Leu Ser Gly
65 70 75 80

Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp
85 90 95

Arg Ser Glu Ser Leu Arg Ala Glu Pro Asn His Cys Leu Tyr Ser Leu
100 105 110

Pro Pro Leu Leu Asp Lys Arg Thr Ser Glu Asp Met Trp Asn Asp Ile
115 120 125

Lys Glu Leu His Ile Leu Tyr His Gln Tyr Ile Ile Asn Val Ser Val
130 135 140

Asp Lys Ser Thr Asn Ala Ile Ser Asn Thr Val Asn Ala Pro Gly Thr
145 150 155 160

Lys Thr Cys Ser Ile Lys Ile Ser Tyr Thr Asn Pro Leu Arg Gln His
165 170 175

Val His Tyr Phe Thr Leu Lys Thr Leu Ile Glu Tyr Tyr Asn Thr Gln
180 185 190

Gln Thr Ser Leu Thr Gly His Arg Ser Ile Asp Asp Gln Gln Glu Ala
195 200 205

Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly
210 215 220

Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu
225 230 235 240

Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln
245 250 255

Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile
260 265 270

Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile
275 280 285

Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn
290 295 300

Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr
305 310 315 320

Gly Thr Ile Ile Ile Lys Asn Asn Met Pro His Asn Glu Arg Glu Ile
325 330 335

Ser Ser Arg Ile Cys Ser Leu Phe Gly Arg Val Ile Ile Asn Gly Arg
340 345 350

Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn
355 360 365

His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile
370 375 380

Thr Ser Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile
385 390 395 400

Phe Glu Ile Ser Arg Asp Thr Ile Leu Asn Ser Thr Asn Tyr Gln Arg
405 410 415

Asn Ile Ser Asn Leu Lys Ile Glu Leu His Asn Pro Asp Glu Gln Leu
420 425 430

Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile
435 440 445

Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His
450 455 460

Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn
465 470 475 480

Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Ile Glu
485 490 495

Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn
500 505 510

Lys Thr Leu Ala Ser Arg Lys Thr
645

<210> 23

<211> 2778

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 23

gatctacaaa taaagtcagc aaaaccacta actataagcc ttcttggcgc atttacaata 60

atatctacat ctatatatat agctttcggg aaatgaagctt ttaatgactt ttggttacca 120

ccactaaatg ttatagatgc atttgatgaa ctatacccat tcatagaagg agctgtagga 180

aatgaaatat aattttttatt tgtaatgtaa ctcacatatt tacaaagatc atttattgtg 240

ccactaccaa aaqatactaa aatatcagca tcttqtgatt tttctgtaat taattctact 300

aacgtttgag atgcacaata tttttgcagg attataaaat ttttaaaagt attaaataca 360

actttattta ataaagcagc agtattttaca tcagctacta taaaagcaca attaccatgc 420
 tgcctaataa tatcacatat gttagaactg attttttctat caatatatat attatctata 480
 atattaacta ctgaacttaa ttcataaaaa tttttatcaa gcaaaacttg ctttagaaac 540
 ttatcataca taataaaaaa acaagctata tgctattatt gtaacttaat agctaagttt 600
 aaaaatctct tatagtaaag tataccaata aaactaaatc ttagaaaaaa ctttctcaaa 660
 tttaaaatat taattttttt tttacaatac gatactagaa cacacacata tattagttaa 720
 ctacaaatac cagtgtactg ctaattcaac atataagtca ttgcttataa taacattatt 780
 aattaaataa taactattct agccagtgtt catcacacta tgtcatttta cagtagatca 840
 caacttaaag aaacaaaata ctattaaaat aacacattaa aagcatatca ataatactta 900
 ataataacca tcaatgttta taattttatgt aaaataaaaa actttttattc ttaatcatta 960
 cactttatgt atatattaca aatttttgaa caataataaa ttaaaactatc aagaatagtt 1020
 gtcattttta gtttatcaca acataggaaa ttctatatcc ctattataag taacatatat 1080
 atttaaataa tacaatcaac aaataaacac actacaactg ataagggttac acctactata 1140
 aacatataga taaataaaaa ttcaacataa ctatcaccaa tataagacaa atactgtttt 1200
 tttgaatata ggaacattaa taacctacta taaatgtttc taactttaag tatagtacaa 1260
 aacaaaatac tcatttttta tttatattaa atatatatat tttaactaca taaattaatt 1320
 accattataa agaaatatat atacttgaga attatcaaaa tattttatctt actatctcaa 1380
 ttaatatagt tgccttatct acataactgc aattgactaa cttatcacag ttgatatgat 1440
 taagaatagc aaaattttac tttatatgtg tttatatgga gactagatgt cagcaaatcc 1500
 cttagatcag tttaggattt ccactatatt caagctacct gatattggcg aatataatat 1560
 tgattttact aatgcctcat tattttatggt attatccaca tttttaatct ctttgtcttg 1620
 ctatgttgga ttaaggaaag aaagtgttat tccgaatcca ttacaatcaa taatagaaat 1680
 tattttatgat tttattggtt ctacaataga aagtaatgta ggtaaggaag gattacaata 1740
 cgtaccatta gtttttacia tattttacatt cattctagta tgtaatctct taggtatatt 1800
 accattaggg ttcactgtaa caagtcatat tgcagtaaca tttgcaatat caatgattgt 1860
 attcataagt gtaacattca taggatttaa acaccaagga actcatttcc ttcatatatt 1920
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ctattgcgca cgccctgtaa gcctatcaat acgactcgct gctaatatga tagctggcca 2040
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tgaaacagaa gataaactaa aaaaatatgt ttatactggg gctgcttttag ttgaagcaat 2460
gggtttatatt tctttcctat tagccctatt actaattttt gtagcctaata gtagatttat 2520
ggacacaata ccacagttag atatatcttc ttatccttct cagttttttt ggtttttttt 2580
atcttttagt gttttgtaca ttataattag taaaaatgtg ctgccaaaga ttgaaaatat 2640
agtaagaaag aggtataata ttataagatg ttctattgat tctgttaagg gtgatttaag 2700
ccatgcgcag caagagttag ataaacagct gctaaagctt actgcagtac aagcagaagt 2760
agatagaatt atacgatc 2778

<210> 24
<211> 551
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
<220>
<221> misc_feature
<222> (1)..(551)
<223> Complement to SEQ ID NO:23, nucleotides <1..551
Hypothetical AraM protein
Product = "9hworfli"

<400> 24
gatctacaaa taaagtcagc aaaaccacta actataagcc ttcttggcgc atttacaata 60
atatctacat ctatatatat agctttcggg aaatgagctt ttaatgactt tttgttacca 120
ccactaaatg ttatagatgc atttgatgaa ctatacccat tcatagaagg agctgtagga 180
aatgaaatat aatttttatt tgtaatgtaa ctcacatatt tacaaagatc atttattgtg 240
ccactaccaa aagatactaa aatatcagca tcttgtgatt tttctgtaat taattctact 300
aacgtttgag atgcacaata tttttgcagg attataaaat ttttaaaagt attaaataca 360

actttattta ataaagcagc agtattttaca tcagctacta taaaagcaca attaccatgc 420
 tgcctaataa tatcacatat gttagaactg atttttctat caatatatat attatctata 480
 atattaacta ctgaacttaa ttcataaaaa tttttatcaa gcaaaacttg ctttagaaac 540
 ttatcataca t 551

<210> 25
 <211> 732
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(732)
 <223> Corresponds to SEQ ID NO:23, nucleotides 1487..2218
 Hypothetical ATP synthase A chain
 Product = "9hworf2"

<400> 25
 atg tca gca aat ccc tta gat cag ttt agg att tcc act ata ttc aag 48
 Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys
 1 5 10 15
 cta cct gat att ggc gaa tat aat att gat ttt act aat gcc tca tta 96
 Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu
 20 25 30
 ttt atg gta tta tcc aca ttt tta atc tcc ttg tct tgc tat gtt gga 144
 Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly
 35 40 45
 tta agg aaa gaa agt gtt att ccg aat cca tta caa tca ata ata gaa 192
 Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu
 50 55 60
 att att tat gat ttt att gtt tct aca ata gaa agt aat gta ggt aag 240
 Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys
 65 70 75 80
 gaa gga tta caa tac gta cca tta gtt ttt aca ata ttt aca ttc att 288
 Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile
 85 90 95
 cta gta tgt aat ctc tta ggt ata tta cca tta ggg ttc act gta aca 336
 Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr
 100 105 110
 agt cat att gca gta aca ttt gca ata tca atg att gta ttc ata agt 384
 Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser
 115 120 125

gta aca ttc ata gga ttt aaa cac caa gga act cat ttc ctt cat ata 432
Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile
130 135 140

ttg tta cca caa ggc aca cca atg tgg tta gca cct atg atg gtc tta 480
Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu
145 150 155 160

att gaa tta ttt gcc tat tgc gca cgc cct gta agc cta tca ata cga 528
Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg
165 170 175

ctc gct gct aat atg ata gct ggc cat act att atc aag gtt ata gca 576
Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala
180 185 190

gga ttc gtt ata aat atg aat ata ttt tta aca cct tta cct ata gca 624
Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala
195 200 205

ttc att ata ata ctt att ggg ttt gaa ata ttc gtt gca atc tta cag 672
Phe Ile Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln
210 215 220

gca tac att ttt aca gta ctc act tgt gtg tac tta tca gat gca gta 720
Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val
225 230 235 240

aat aag cac taa 732
Asn Lys His

<210> 26

<211> 243

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 26

Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys
1 5 10 15

Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu
20 25 30

Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly
35 40 45

Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu
50 55 60

Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys
65 70 75 80

Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile
85 90 95

Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr
100 105 110

Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser
115 120 125

Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile
130 135 140

Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu
145 150 155 160

Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg
165 170 175

Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala
180 185 190

Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala
195 200 205

Phe Ile Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln
210 215 220

Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val
225 230 235 240

Asn Lys His

<210> 27

<211> 222

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

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T:\Sequences\UF\UF-299XC1\As-Filed-Seq-List.txt/DNB/jaj

<210> 29
 <211> 261
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(261)
 <223> Corresponds to SEQ ID NO:23, nucleotides 2519..>2778
 Hypothetical ATP synthase B chain
 Product="9hworf4i"

<220>
 <221> misc_feature
 <222> (261)..(261)
 <223> n = a, c, g, or t

<400> 29
 atg gac aca ata cca cag tta gat ata tct tct tat cct tct cag ttt 48
 Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe
 1 5 10 15
 ttt tgg ttt ttt tta tct ttt agt gtt ttg tac att ata att agt aaa 96
 Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ile Ser Lys
 20 25 30
 aat gtg ctg cca aag att gaa aat ata gta aga aag agg tat aat att 144
 Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile
 35 40 45
 ata aga tgt tct att gat tct gtt aag ggt gat tta agc cat gcg cag 192
 Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln
 50 55 60
 caa gag tta gat aaa cag ctg cta aag ctt act gca gta caa gca gaa 240
 Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu
 65 70 75 80
 gta gat aga att ata cga tcn 261
 Val Asp Arg Ile Ile Arg Xaa
 85

<210> 30
 <211> 87
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (87)..(87)
 <223> The 'Xaa' at location 87 stands for Ser.

<220>
 <221> misc_feature
 <222> (261)..(261)
 <223> n = a, c, g, or t

<400> 30

Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe
 1 5 10 15

Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ile Ser Lys
 20 25 30

Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile
 35 40 45

Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln
 50 55 60

Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu
 65 70 75 80

Val Asp Arg Ile Ile Arg Xaa
 85

<210> 31
 <211> 3814
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 31
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 gggaggcggg ggaagagcct gcatcattcc ggcaactcgg gcgcgaaggc gaacaggtcc 180
 gacggccgca cgaacagtcc caggcccatc tggatgccga ccagcaggac gatcagcgcc 240
 agaagcatac gcagtacgtc cggccggaac cggcccgaca gcctcgcccc gtactggggc 300
 cccacgaccc caccgaccag caggatgggtc gacaggacga tgctgacggc ctggttgagg 360
 cccgcctgaa gaatggtggt catggcggtg acgatgatga tctggaacag gctggtgccc 420
 accacgaccc cggccttcat ccgcagcaca tagagcatgg ccggcaccag aatgaagccg 480
 ccgcccaccc ccatgatggc ggacaacaca ccggcgaaac cgcccagcgc gaacggggga 540

atggcgctga ttagagggcc cgagcggggg aagcgcatct tcagcggcag gccatacagc 600
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 cagaagctcg gtaccgacac ccgggcccgc ggccttttcg accgcgtcca tccgctggcg 3480
 cagttcattg acgcccagac gttgacgctc ctgatatcg tagaggcggc ccgccagcgc 3540
 ccccatggtg gtctcgacct tgctgaaggc ctccggcggtc tgagggcccg ttctctgctc 3600
 gaaccggcgc agacgcttgt gcccctcgcg caactcctcg gcgatgtcgt caatgcgacg 3660
 accataggcc ctgcccgcgt cgtcctgccc ctccagtcgg cggacaaggc ccgagacggc 3720
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 gatggcatcg accgagggcc cgaggcgcgt gatc 3814

<210> 32
 <211> 810
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(810)
 <223> Complement to SEQ ID NO:31, nucleotides 144..953
 Similar to gas vesicle protein
 Product = "l2hworf1"

<400> 32
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 gcccatctgg atgccgacca gcaggacgat cagcgccaga agcatacgca gtacgtccgg 120
 ccggaaccgg cccgacagcc tcgccccgta ctgggcccc acgacccac cgaccagcag 180
 gatggtcgac aggacgatgt cgacgggtctg gttgcggccc gcctgaagaa tgggtggcat 240
 ggcggtgacg atgatgatct ggaacaggct ggtgcccacc acgaccccg ccttcacccg 300
 cagcacatag agcatggccg gcaccagaat gaagccgccc cccaccccca tgatggcgga 360
 caacacaccg gcgaaaccgc ccagcgcgaa cgggggaatg gcgctgatgt agaggcccga 420
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<210> 33
 <211> 2638
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(2638)
 <223> Complement to SEQ ID NO:31, nucleotides 1177..>3814
 Hypothetical polar organelle development protein

Product = "12hworf2i"

<400> 33

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aatgccgacg tctccgggtct catagagttt ggcgacgttg aactggccat cgaccagtcc	240
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<210> 34
<211> 1698
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(1698)
<223> Corresponds to SEQ ID NO:31, nucleotides 1594..3291
Product = "12hworf3"

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ggc ggc ctg ctt cag ggt ctc gac tgc ggc ggc gtc ctc ggc gtc cag	96
Gly Gly Leu Leu Gln Gly Leu Asp Cys Gly Gly Val Leu Gly Val Gln	
20 25 30	
ctg gac cat cgc ctg ctg gta gag cac ctc tcc gcg ggc cag atc ctc	144
Leu Asp His Arg Leu Leu Val Glu His Leu Ser Ala Gly Gln Ile Leu	
35 40 45	
ggg cgc agg ctc gct cgg aac aat ggc cag ggc tgc gat cgg ttg agc	192
Gly Arg Arg Leu Ala Arg Asn Asn Gly Gln Gly Cys Asp Arg Leu Ser	
50 55 60	
ggt ttc ccc cgc tgt cgg cag gcc ggc aat att cag gcc cga tcc cgt	240
Gly Phe Pro Arg Cys Arg Gln Ala Gly Asn Ile Gln Ala Arg Ser Arg	
65 70 75 80	
cag ctg tcc ggt cgc ata ggc ccc gcc ggc ggt cag cag cac ggc aat	288
Gln Leu Ser Gly Arg Ile Gly Pro Ala Gly Gly Gln Gln His Gly Asn	
85 90 95	
ggc cga agc gcc gag cgc ctt gcg aac cgt gcc acc gtc ctt gcc cgc	336
Gly Arg Ser Ala Glu Arg Leu Ala Asn Arg Ala Thr Val Leu Ala Arg	
100 105 110	
ctg ctt ttc cag ccg ttc ctg aag acg gga ctt gcc gcc gcg ctt cag	384
Leu Leu Phe Gln Pro Phe Leu Lys Thr Gly Leu Ala Ala Ala Leu Gln	
115 120 125	
gcc gaa gcc cga acg ggc cgg agc ctc gac ggc ggc agc cgc cat ggc	432
Ala Glu Ala Arg Thr Gly Arg Ser Leu Asp Gly Gly Ser Arg His Gly	
130 135 140	
cgc acg ggc ggc gtc gat ggt ctg gcg ggt cga gga ggc gcg acc ctg	480
Arg Thr Gly Gly Val Asp Gly Leu Ala Gly Arg Gly Gly Ala Thr Leu	
145 150 155 160	
ggc cgc cgc agc gcg cag ggc ccg cgg atc gac gaa gtc cgt ttc gcc	528
Gly Arg Arg Ser Ala Gln Gly Pro Arg Ile Asp Glu Val Arg Phe Ala	
165 170 175	
gtc gaa atc gtc atg acc gcc gtc aaa ggc cga cgg ggt cct gtt tcc	576
Val Glu Ile Val Met Thr Ala Val Lys Gly Arg Arg Gly Pro Val Ser	
180 185 190	
ggg cgc ggt cgc ctc caa ggc atc cga gac gtc cgc acc gcc gaa gcc	624
Gly Arg Gly Arg Leu Gln Gly Ile Arg Asp Val Arg Thr Ala Glu Ala	
195 200 205	
ctg gcc gaa agc gac cgg agc agc cgg gat ctg aac cgg cgg agc atc	672
Leu Ala Glu Ser Asp Arg Ser Ser Arg Asp Leu Asn Arg Arg Ser Ile	
210 215 220	
gac cgg ggc cgg ctg ggt ggc cgc gaa cgg tgg cgg cgt gaa ggc ggc	720
Asp Arg Gly Arg Leu Gly Gly Arg Glu Arg Trp Arg Arg Glu Gly Gly	
225 230 235 240	

gat ctg cgg cgg cgg gcc gac ttc ctc ggc cag cga ggt cat ggt ggg Asp Leu Arg Arg Arg Ala Asp Phe Leu Gly Gln Arg Gly His Gly Gly	768
245 250 255	
tcg gct gcc gaa cgg cat cgg agc ggc gac ggg tac ctc tgc ggt cgg Ser Ala Ala Glu Arg His Arg Ser Gly Asp Gly Tyr Leu Cys Gly Arg	816
260 265 270	
tgc gag gtc ctc atc cac gcg ggg gcc gcg cat gac cgc gtc gaa gat Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp	864
275 280 285	
ggc gtc ggc ggt cag gac ctc ggg ggt cgc gcg ctc gac agg gaa ggg Gly Val Gly Gly Gln Asp Leu Gly Gly Arg Ala Leu Asp Arg Glu Gly	912
290 295 300	
cgc ggg gtc cgg ctc ggg cgg agc cag att cgc gga cca ggc ctg ctg Arg Gly Val Arg Leu Gly Arg Ser Gln Ile Arg Gly Pro Gly Leu Leu	960
305 310 315 320	
ctc ggc ata gat cgg gtc gtc gaa gac tgc gtc cga gaa agg cgc atc Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile	1008
325 330 335	
ggg gaa ggc tgt gtc cgg aaa ggc cgc ggc ccg cca atc ggg ttc cgg Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg	1056
340 345 350	
cac ggc ggc gac cgc agt cgg aac ttc ggc ccg gcg ttc gat att gcc His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala	1104
355 360 365	
acg cgc ctc ggc gat cag ggc cgc cgt gcg ctc ttc cga cat ccg cat Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His	1152
370 375 380	
ccg ctc ggc cag ttc gcc gga agc gcg gtc gta gcc ctg ctc gat gcg Pro Leu Gly Gln Phe Ala Gly Ser Ala Val Val Ala Leu Leu Asp Ala	1200
385 390 395 400	
ggc gga act gtc ggc gag acg gcg gcc gat atc gtc cag cgc ctg ctg Gly Gly Thr Val Gly Glu Thr Ala Ala Asp Ile Val Gln Arg Leu Leu	1248
405 410 415	
cga ccg ccg ctc cga ctg ggc gat gcg ttc gct cag ccg gtc gga gat Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp	1296
420 425 430	
acg ggt gat ctc ccc gcc cag ttt ttc cag ggc cag ggc atg ccg gtc Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val	1344
435 440 445	
gtc ggt cgc gat cag tcg ctg ttc gat gcc ctg ggc gaa gcg gcc cat Val Gly Arg Asp Gln Ser Leu Phe Asp Ala Leu Gly Glu Ala Ala His	1392

450 455 460
 gtc ggt ctc gac ctt gcg gct cag ctg ttc gaa acg ggc cgg aac ctc 1440
 Val Gly Leu Asp Leu Ala Ala Gln Leu Phe Glu Thr Gly Arg Asn Leu
 465 470 475 480
 ggt ctc gat cga ctg gac ccg acc att cag gtt ctg ggc gat gcg cag 1488
 Gly Leu Asp Arg Leu Asp Pro Thr Ile Gln Val Leu Gly Asp Ala Gln
 485 490 495
 aac ctc gcg ccc cat cgc ctc gac cgc ctt ggc gga gcg ttc ctc cga 1536
 Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg
 500 505 510
 cgc ctt gac ctg ctc gcc gat ggc cag gac cgc gcg ctc gat ccg gtc 1584
 Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val
 515 520 525
 cat ccg gcc ttc ggt ttc ggc tgt atc gag ccg ccg cat cat ctc ggc 1632
 His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly
 530 535 540
 gcg att ggc ttc aac cga ccg gct cag ggt ctc ggc gag ctt ttc gaa 1680
 Ala Ile Gly Phe Asn Arg Pro Ala Gln Gly Leu Gly Glu Leu Phe Glu
 545 550 555 560
 gcg ggc ggc ctc gcg tga 1698
 Ala Gly Gly Leu Ala
 565
 <210> 35
 <211> 565
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <400> 35
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 Leu Asp His Arg Leu Leu Val Glu His Leu Ser Ala Gly Gln Ile Leu
 35 40 45
 Gly Arg Arg Leu Ala Arg Asn Asn Gly Gln Gly Cys Asp Arg Leu Ser
 50 55 60
 Gly Phe Pro Arg Cys Arg Gln Ala Gly Asn Ile Gln Ala Arg Ser Arg

65 70 75 80
 Gln Leu Ser Gly Arg Ile Gly Pro Ala Gly Gly Gln Gln His Gly Asn
 85 90 95
 Gly Arg Ser Ala Glu Arg Leu Ala Asn Arg Ala Thr Val Leu Ala Arg
 100 105 110
 Leu Leu Phe Gln Pro Phe Leu Lys Thr Gly Leu Ala Ala Ala Leu Gln
 115 120 125
 Ala Glu Ala Arg Thr Gly Arg Ser Leu Asp Gly Gly Ser Arg His Gly
 130 135 140
 Arg Thr Gly Gly Val Asp Gly Leu Ala Gly Arg Gly Gly Ala Thr Leu
 145 150 155 160
 Gly Arg Arg Ser Ala Gln Gly Pro Arg Ile Asp Glu Val Arg Phe Ala
 165 170 175
 Val Glu Ile Val Met Thr Ala Val Lys Gly Arg Arg Gly Pro Val Ser
 180 185 190
 Gly Arg Gly Arg Leu Gln Gly Ile Arg Asp Val Arg Thr Ala Glu Ala
 195 200 205
 Leu Ala Glu Ser Asp Arg Ser Ser Arg Asp Leu Asn Arg Arg Ser Ile
 210 215 220
 Asp Arg Gly Arg Leu Gly Gly Arg Glu Arg Trp Arg Arg Glu Gly Gly
 225 230 235 240
 Asp Leu Arg Arg Arg Ala Asp Phe Leu Gly Gln Arg Gly His Gly Gly
 245 250 255
 Ser Ala Ala Glu Arg His Arg Ser Gly Asp Gly Tyr Leu Cys Gly Arg
 260 265 270
 Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp
 275 280 285

Gly Val Gly Gly Gln Asp Leu Gly Gly Arg Ala Leu Asp Arg Glu Gly
290 295 300

Arg Gly Val Arg Leu Gly Arg Ser Gln Ile Arg Gly Pro Gly Leu Leu
305 310 315 320

Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile
325 330 335

Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg
340 345 350

His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala
355 360 365

Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His
370 375 380

Pro Leu Gly Gln Phe Ala Gly Ser Ala Val Val Ala Leu Leu Asp Ala
385 390 395 400

Gly Gly Thr Val Gly Glu Thr Ala Ala Asp Ile Val Gln Arg Leu Leu
405 410 415

Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp
420 425 430

Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val
435 440 445

Val Gly Arg Asp Gln Ser Leu Phe Asp Ala Leu Gly Glu Ala Ala His
450 455 460

Val Gly Leu Asp Leu Ala Ala Gln Leu Phe Glu Thr Gly Arg Asn Leu
465 470 475 480

Gly Leu Asp Arg Leu Asp Pro Thr Ile Gln Val Leu Gly Asp Ala Gln
485 490 495

Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg
500 505 510

Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val
515 520 525

His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly
530 535 540

Ala Ile Gly Phe Asn Arg Pro Ala Gln Gly Leu Gly Glu Leu Phe Glu
545 550 555 560

Ala Gly Gly Leu Ala
565

<210> 36
<211> 546
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(546)
<223> Corresponds to SEQ ID NO:31, nucleotides 2789..3334
Product = "12hworf4"

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tgc tgc gac cgc cgc tcc gac tgg gcg atg cgt tcg ctc agc cgg tcg 96
Cys Cys Asp Arg Arg Ser Asp Trp Ala Met Arg Ser Leu Ser Arg Ser
20 25 30

gag ata cgg gtg atc tcc ccg ccc agt ttt tcc agg gcc agg gca tgc 144
Glu Ile Arg Val Ile Ser Pro Pro Ser Phe Ser Arg Ala Arg Ala Cys
35 40 45

cgg tcg tcg gtc gcg atc agt cgc tgt tcg atg ccc tgg gcg aag cgg 192
Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg
50 55 60

ccc atg tcg gtc tcg acc ttg cgg ctc agc tgt tcg aaa cgg gcc gga 240
Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly
65 70 75 80

acc tcg gtc tcg atc gac tgg acc cga cca ttc agg ttc tgg gcg atg 288
Thr Ser Val Ser Ile Asp Trp Thr Arg Pro Phe Arg Phe Trp Ala Met
85 90 95

cgc aga acc tcg cgc ccc atc gcc tcg acc gcc ttg gcg gag cgt tcc 336

Arg Arg Thr Ser Arg Pro Ile Ala Ser Thr Ala Leu Ala Glu Arg Ser
 100 105 110

tcc gac gcc ttg acc tgc tcg ccg atg gcc agg acc gcg cgc tcg atc 384
 Ser Asp Ala Leu Thr Cys Ser Pro Met Ala Arg Thr Ala Arg Ser Ile
 115 120 125

cgg tcc atc cgg cct tcg gtt tcg gct gta tcg agc cgc cgc atc atc 432
 Arg Ser Ile Arg Pro Ser Val Ser Ala Val Ser Ser Arg Arg Ile Ile
 130 135 140

tcg gcg cga ttg gct tca acc gac cgg ctc agg gtc tcg gcg agc ttt 480
 Ser Ala Arg Leu Ala Ser Thr Asp Arg Leu Arg Val Ser Ala Ser Phe
 145 150 155 160

tcg aag cgg gcg gcc tcg cgt gag ccc tcg ggc tcg acc cgg gac tcg 528
 Ser Lys Arg Ala Ala Ser Arg Glu Pro Ser Gly Ser Thr Arg Asp Ser
 165 170 175

gcg gcg cgc agc cgc tga 546
 Ala Ala Arg Ser Arg
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<210> 37

<211> 181

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 37

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Cys Cys Asp Arg Arg Ser Asp Trp Ala Met Arg Ser Leu Ser Arg Ser
 20 25 30

Glu Ile Arg Val Ile Ser Pro Pro Ser Phe Ser Arg Ala Arg Ala Cys
 35 40 45

Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg
 50 55 60

Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly
 65 70 75 80

Thr Ser Val Ser Ile Asp Trp Thr Arg Pro Phe Arg Phe Trp Ala Met
 85 90 95

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 aagttatatg gagtggaaga ttgaatcctt acctgtacct tatgataaag ctatgtgttt 3600
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 tgaacatttt ccgttatata cggctggtac tagtgcaagg agtgaggaat tactaaccga 3720
 tagtttattt cctgtatatt ctacaggtag aggtggtaaa tacacttatc atggctcctgg 3780
 tcaaagaatt gcttatgtga tgatggattt aaaagcaaga gataaatgta atgttagggt 3840
 gtatgttgaa actttgggtg agtggattgt taaaacttta aagcattttt caatacgatc 3900

n

3901

<210> 39
 <211> 1503
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

 <220>
 <221> CDS
 <222> (1)..(1503)
 <223> Corresponds to SEQ ID NO:38, nucleotides 816..2318
 Hypothetical cytosol aminopeptidase
 Product = "13hworf1"

<400> 39
 atg ata aat gta tca ttt ttg ggt tta atg tct gga ata tct gta tta 48
 Met Ile Asn Val Ser Phe Leu Gly Leu Met Ser Gly Ile Ser Val Leu
 1 5 10 15

 tta aag acc acg gta ata gtt gta ggt att ttt gaa gga agt aat cat 96
 Leu Lys Thr Thr Val Ile Val Val Gly Ile Phe Glu Gly Ser Asn His
 20 25 30

 ttg gag gat aat ggt gct tta gaa ggt tat aat gat aaa atc atg gaa 144
 Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu
 35 40 45

 ata gta aat ggt tat caa tct ttt gat ggt aag ttt gct gag gta tta 192
 Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu
 50 55 60

 cct att att ggg tta gag aaa gat ttt cct gtt gtg gta gtt att gga 240
 Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly
 65 70 75 80

 ctg ggt aaa tct gag gat ttt gat gaa aat aaa gct tta aaa gtt ggt 288
 Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly
 85 90 95

 ggt gta ata tat tct gaa ctt aat aga atg aag gta cca gat gca tca 336
 Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser
 100 105 110

 att gtt att aat act gat agt aat gta agt gcc aat att ggt tat gga 384
 Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly
 115 120 125

 gca ctt tta cgt agt ttt aaa ttt gat aaa tat ttc gta gag aaa aaa 432
 Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys
 130 135 140

 gat aaa aat tca gtt tat ttg aat aag ttg ctt cta ttt tca aag agt 480

Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser
 145 150 155 160

gat cca caa gag gtt act gct ttg ttt aat gat tta aaa gct gaa ggt 528
 Asp Pro Gln Glu Val Thr Ala Leu Phe Asn Asp Leu Lys Ala Glu Gly
 165 170 175

gag tca ata ttc tta gct cgt tct ttt gtt tca gag cct ccg aat att 576
 Glu Ser Ile Phe Leu Ala Arg Ser Phe Val Ser Glu Pro Pro Asn Ile
 180 185 190

tta tat cca gaa acg tat gct cag atg ata tat gaa gaa tta agt aag 624
 Leu Tyr Pro Glu Thr Tyr Ala Gln Met Ile Tyr Glu Glu Leu Ser Lys
 195 200 205

gtt ggt gta aca gtt gaa gtc ttt gat gaa gat tac atg aaa gca aat 672
 Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn
 210 215 220

caa atg atg gca ctt ctt gga gta ggt cag ggt agt gct aaa aaa tct 720
 Gln Met Met Ala Leu Leu Gly Val Gly Gln Gly Ser Ala Lys Lys Ser
 225 230 235 240

cga ctt gta gtt atg aaa tgg aat gga ggt gat gag tca gaa agt cct 768
 Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro
 245 250 255

att gcg ttt gtt gga aaa ggt gta act ttt gat act ggt gga ata tcc 816
 Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser
 260 265 270

tta aaa cct tca aag ggt atg tgg gat atg aaa tat gat atg gca ggt 864
 Leu Lys Pro Ser Lys Gly Met Trp Asp Met Lys Tyr Asp Met Ala Gly
 275 280 285

tct gct tct gtt gtt gga att atg cgt act ctt gct gca agg aag gca 912
 Ser Ala Ser Val Val Gly Ile Met Arg Thr Leu Ala Ala Arg Lys Ala
 290 295 300

aaa gtt aat gct gtt gga gtg gtt gga tta gtt gaa aat tca gta gat 960
 Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp
 305 310 315 320

gga aat gcg caa aga cct agt gat gtt gtt att tca atg tct gga caa 1008
 Gly Asn Ala Gln Arg Pro Ser Asp Val Val Ile Ser Met Ser Gly Gln
 325 330 335

aca att gag gtg tta aat act gat gca gag ggt agg ttg gtt tta gct 1056
 Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala
 340 345 350

gat gct tta tgg tat act cag gag atg ttt act cct aaa tta atg gtg 1104
 Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val
 355 360 365

gat tta gca aca tta act ggt gca gta gtg gtt gct tta ggt aat aat 1152
Asp Leu Ala Thr Leu Thr Gly Ala Val Val Val Ala Leu Gly Asn Asn
370 375 380

cag tat gct ggg ctt ttt tca aat gat gat tct att gca aat cag ttg 1200
Gln Tyr Ala Gly Leu Phe Ser Asn Asp Asp Ser Ile Ala Asn Gln Leu
385 390 395 400

att gta gct ggg aat gaa tct ggt gag aaa tta tgg cgg tta cct tta 1248
Ile Val Ala Gly Asn Glu Ser Gly Glu Lys Leu Trp Arg Leu Pro Leu
405 410 415

gat gaa gcc tat gat aaa ctt ata gat tca tca att gct gat atg cag 1296
Asp Glu Ala Tyr Asp Lys Leu Ile Asp Ser Ser Ile Ala Asp Met Gln
420 425 430

aat att tca aca aaa gga tat ggg gcg gat agt att act gca gca cag 1344
Asn Ile Ser Thr Lys Gly Tyr Gly Ala Asp Ser Ile Thr Ala Ala Gln
435 440 445

ttc tta caa aga ttt gtt aat ggt gtt cct tgg gtg cat ttg gat att 1392
Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile
450 455 460

gct ggt atg gca tgg gat tat gaa ggc act gag ata tgt cct aag ggt 1440
Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly
465 470 475 480

gca act ggt ttt ggg gta agg cta tta aat aga ttt gta tca aag tac 1488
Ala Thr Gly Phe Gly Val Arg Leu Leu Asn Arg Phe Val Ser Lys Tyr
485 490 495

tat gag tct cat tag 1503
Tyr Glu Ser His
500

<210> 40

<211> 500

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 40

Met Ile Asn Val Ser Phe Leu Gly Leu Met Ser Gly Ile Ser Val Leu
1 5 10 15

Leu Lys Thr Thr Val Ile Val Val Gly Ile Phe Glu Gly Ser Asn His
20 25 30

Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu
35 40 45

Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu
50 55 60

Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly
65 70 75 80

Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly
85 90 95

Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser
100 105 110

Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly
115 120 125

Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys
130 135 140

Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser
145 150 155 160

Asp Pro Gln Glu Val Thr Ala Leu Phe Asn Asp Leu Lys Ala Glu Gly
165 170 175

Glu Ser Ile Phe Leu Ala Arg Ser Phe Val Ser Glu Pro Pro Asn Ile
180 185 190

Leu Tyr Pro Glu Thr Tyr Ala Gln Met Ile Tyr Glu Glu Leu Ser Lys
195 200 205

Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn
210 215 220

Gln Met Met Ala Leu Leu Gly Val Gly Gln Gly Ser Ala Lys Lys Ser
225 230 235 240

Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro
245 250 255

Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser
260 265 270

Leu Lys Pro Ser Lys Gly Met Trp Asp Met Lys Tyr Asp Met Ala Gly
 275 280 285

Ser Ala Ser Val Val Gly Ile Met Arg Thr Leu Ala Ala Arg Lys Ala
 290 295 300

Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp
 305 310 315 320

Gly Asn Ala Gln Arg Pro Ser Asp Val Val Ile Ser Met Ser Gly Gln
 325 330 335

Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala
 340 345 350

Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val
 355 360 365

Asp Leu Ala Thr Leu Thr Gly Ala Val Val Val Ala Leu Gly Asn Asn
 370 375 380

Gln Tyr Ala Gly Leu Phe Ser Asn Asp Asp Ser Ile Ala Asn Gln Leu
 385 390 395 400

Ile Val Ala Gly Asn Glu Ser Gly Glu Lys Leu Trp Arg Leu Pro Leu
 405 410 415

Asp Glu Ala Tyr Asp Lys Leu Ile Asp Ser Ser Ile Ala Asp Met Gln
 420 425 430

Asn Ile Ser Thr Lys Gly Tyr Gly Ala Asp Ser Ile Thr Ala Ala Gln
 435 440 445

Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile
 450 455 460

Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly
 465 470 475 480

Ala Thr Gly Phe Gly Val Arg Leu Leu Asn Arg Phe Val Ser Lys Tyr

485

490

495

Tyr Glu Ser His
500

<210> 41
<211> 639
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> CDS
<222> (1)..(639)
<223> Corresponds to SEQ ID NO:38, nucleotides 2486..3124
Hypothetical phosphoribosylamine-glycine ligase
Product = "13hworf2"

<400> 41
atg act atg aaa cca ctt agg tta ggt att tta att tca ggt agg ggt 48
Met Thr Met Lys Pro Leu Arg Leu Gly Ile Leu Ile Ser Gly Arg Gly
1 5 10 15

tct aat atg cag gct ctg att aat gct tgt cag cga gat gat ttt cct 96
Ser Asn Met Gln Ala Leu Ile Asn Ala Cys Gln Arg Asp Asp Phe Pro
20 25 30

gca agt gta tcc tgt gtt ata tca aat aaa tca aat gca aac ggt cta 144
Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu
35 40 45

ata ctt gct cag caa agt aat att aaa act ttt ata gta caa ggt cgt 192
Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg
50 55 60

cct cta gat ttt gat gct att gat aat ata ctt gaa gaa cat gag gtg 240
Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val
65 70 75 80

gat tta atc tgt ctt gca gga ttt atg agt att gtt cct gaa aag ttt 288
Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe
85 90 95

att aat aag tgg tta tat aag gtt att aat ata cat cct tct ctc ttg 336
Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu
100 105 110

cca tca ttt aag ggt tta aat gca caa gct caa gca tta aag gct gga 384
Pro Ser Phe Lys Gly Leu Asn Ala Gln Ala Gln Ala Leu Lys Ala Gly
115 120 125

gta aag att gct gga tgt aca gtt cat tat gta tac cca gaa gtt gat 432
Val Lys Ile Ala Gly Cys Thr Val His Tyr Val Tyr Pro Glu Val Asp

130 135 140

ggt gga cct att att gtt cag gca gca gtt cca gtg ttt tca tct gat 480
 Gly Gly Pro Ile Ile Val Gln Ala Ala Val Pro Val Phe Ser Ser Asp
 145 150 155 160

agt gtt gag gat ctt gct aat aga ata ttg aag atg gaa cat att tgt 528
 Ser Val Glu Asp Leu Ala Asn Arg Ile Leu Lys Met Glu His Ile Cys
 165 170 175

tac cct aaa gct gtg gaa cta att gct tat aat cag cta caa ctt aac 576
 Tyr Pro Lys Ala Val Glu Leu Ile Ala Tyr Asn Gln Leu Gln Leu Asn
 180 185 190

ggt agt tta gct tta tca gca aaa aca cta cac atg ttt tat aat gat 624
 Gly Ser Leu Ala Leu Ser Ala Lys Thr Leu His Met Phe Tyr Asn Asp
 195 200 205

gaa gct ttt gta tag 639
 Glu Ala Phe Val
 210

<210> 42
 <211> 212
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 42

Met Thr Met Lys Pro Leu Arg Leu Gly Ile Leu Ile Ser Gly Arg Gly
 1 5 10 15

Ser Asn Met Gln Ala Leu Ile Asn Ala Cys Gln Arg Asp Asp Phe Pro
 20 25 30

Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu
 35 40 45

Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg
 50 55 60

Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val
 65 70 75 80

Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe
 85 90 95

Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu

100

105

110

Pro Ser Phe Lys Gly Leu Asn Ala Gln Ala Gln Ala Leu Lys Ala Gly
 115 120 125

Val Lys Ile Ala Gly Cys Thr Val His Tyr Val Tyr Pro Glu Val Asp
 130 135 140

Gly Gly Pro Ile Ile Val Gln Ala Ala Val Pro Val Phe Ser Ser Asp
 145 150 155 160

Ser Val Glu Asp Leu Ala Asn Arg Ile Leu Lys Met Glu His Ile Cys
 165 170 175

Tyr Pro Lys Ala Val Glu Leu Ile Ala Tyr Asn Gln Leu Gln Leu Asn
 180 185 190

Gly Ser Leu Ala Leu Ser Ala Lys Thr Leu His Met Phe Tyr Asn Asp
 195 200 205

Glu Ala Phe Val
 210

<210> 43
 <211> 354
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(351)
 <223> Corresponds to SEQ ID NO:38, nucleotides 3548...>3900
 Hypothetical lipoate-protein ligase B
 Product = "13hworf3i"

<220>
 <221> misc_feature
 <222> (354)..(354)
 <223> n = a, c, g, or t

<220>
 <221> misc_feature
 <222> (352)..(354)
 <223> Xaa = Ser

<400> 43
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 1 5 10 15

 tgt ttt atg caa caa agg gtc gag ggt att gct aat aag aca caa gat 96
 Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp
 20 25 30

 gaa cta gta tgg tta ctt gaa cat ttt ccg tta tat acg gct ggt act 144
 Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr
 35 40 45

 agt gca agg agt gag gaa tta cta acc gat agt tta ttt cct gta tat 192
 Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr
 50 55 60

 tct aca ggt aga ggt ggt aaa tac act tat cat ggt cct ggt caa aga 240
 Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg
 65 70 75 80

 att gct tat gtg atg atg gat tta aaa gca aga gat aaa tgt aat gtt 288
 Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val
 85 90 95

 agg ttg tat gtt gaa act ttg ggt gag tgg att gtt aaa act tta aag 336
 Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys
 100 105 110

 cat ttt tca ata cga tcn 354
 His Phe Ser Ile Arg
 115

<210> 44
 <211> 117
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (354)..(354)
 <223> n = a, c, g, or t

<220>
 <221> misc_feature
 <222> (352)..(354)
 <223> Xaa = Ser

<400> 44

 Met Glu Trp Lys Ile Glu Ser Leu Pro Val Pro Tyr Asp Lys Ala Met
 1 5 10 15

Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp
20 25 30

Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr
35 40 45

Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr
50 55 60

Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg
65 70 75 80

Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val
85 90 95

Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys
100 105 110

His Phe Ser Ile Arg
115

<210> 45

<211> 4369

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 45

gacacctga ttgaggaaga tcaacaccac aatgtttttc tttagtgtga tacataacat 60

gacaggata gaaactaggc actaacttac tagttgcctc ttcgtatata ggattaccat 120

ttctgtcaaa atctaactt aaagaacaag tttcacttaa accacgagta tttcttaaac 180

tatcttcaac agtattaacc aaattcaaac ttgaaactaa ttggaacgta ctttcttttc 240

caacacatat aacaggctta ctatccttaa cagtagtttc acaactagaa gcagataaaa 300

ctgaatcctc tattttacct aaatctacac ctgatagttt tactttatca tcttttacct 360

taccactttg aaaattaaaa gtagcaccaa cacttctagc aacactactg tccttttcat 420

ctcttatagc agtaccttca gatactactt ttttctctac agatttatcc ttagtactac 480

ctgtacactc tgtatcagta acatcccttt tctcatctgg tttctctaata ctagaaccag 540

ataatctaac ttgattactt ttcatatcac cagtttgagc actcgactt acaaaaacat 600

ctctctttttt ttcatttatt cttatagtat caccttcagg tactactttt ttctctacag 660
 atttatcctt agtatcaacc ataacatcag atttaaaact aagacttggt tttatagtag 720
 tttcagtatg actatagtga acaccaacac cagcattttt cttaaccata acttggtgac 780
 cttctacact atcgcgttct acagtttgaa cgtcagaaat ttgatgtgtt acctgatcca 840
 ttttggtaga tgagacagta gattttgatt ttaaaacatg acctatatca tcactatcat 900
 tatggtaaac tgattttaga aattcaatac catcttttcc agataaagtg tccatttcgt 960
 acttttcata ttcactctga ctacaataag taaccctact ttttgatatca ttatctgata 1020
 tatctaattc tcttgactta tacttcataa cactcaacac ataacataca aacctaacca 1080
 caagcagaac atagtaaaca catataaaaa acagcgacac tgctgtgtat aggattatct 1140
 cattcatatt atttaataag aaaattaata taagttaata tatacatata tatttaacaa 1200
 ctaaaagaat tataataaaa aaatttacta tttctaatat ttttttaatt agttactaaa 1260
 tctatattat attttttaaat aatactaatt tttaatataa ataaactaat atcaaatgat 1320
 aatcttttac tatattagca acatcataaa gtgctaaata ctacttctta tagaggatga 1380
 tctactatca ctcattacac aactcacatt aatataagat ggtaaccttt ctgaaggagt 1440
 atatatttta ttcttcttaa cccgttttac aacattactt ataataatag catctgaaat 1500
 ttctcccata ttgtttttta aatattcttt aactacaaca gcagcttttt tctccatctt 1560
 atcactaaaa aatgaagcca atttctgaat agatttcaat atatcaagtt cccatttatc 1620
 attatttatc accttagaca ttaatgtacc aaacactgaa ctttgagaat gatttccatg 1680
 ttctagatat ctggttacca tattatgtac agccctatat ttaagtcgca ttttactaac 1740
 cgccatgatc aaaacattct tatatgctac tgtgatcgct tctttttgaa tactctcata 1800
 tacttggtgtg acatattcag aatacatata agattttact tgattctcta attcacagat 1860
 caaaaaactct cgatcacagg gattagcatc acatactctc atatcctttg ccaataagta 1920
 aacacattct tttataagtc ctgcttttaga ctttttatac aatggtgtac cacgctgaat 1980
 agcaaagtcc cgtatcataa caggcattac ttgtttatcc atacgttgta tagtattcaa 2040
 catcagacta tatgcatcca tacattcatg cttaacttta ctacgtaaata tctcatcacc 2100
 tattcccgac aacagagtat ctagtctatc actctcaata ttccatgctg atatcaataa 2160
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 gtcacattca tcatctctaa acaagtatgt agtagtactt aaaccttgct tcttctttaa 2280

cttatctgta ttcaaacaag tagactcttg acctataact ctaccttcac tttcaatact 2340
 atgtttttaca gatggtaata cagtacaatc tacactactt tcattttttc tacttttcacg 2400
 aacacgatta gtatcatgaa taccacctat tttactagaa gccacactaa ttttctggcc 2460
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 tctcctacta cgtcatcag catctttaac atgcctagca tcactcttct taccagtaac 2580
 tgacctaaact gcttgatcac aaacaaccaa tctcttacta ttagcatgta cttttttatc 2640
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 cattatagct tctcgaaaaa cttgcggatt actaaaaatc aaggacatac tagtcattgg 2760
 atcattaaac atcaaataca tattaattcg tggattacta aacattaagc ttacattcag 2820
 acacacattt gacaatagtt tgaatagatt ttcacagttc atacttgtca tctgacttaa 2880
 caattgttga tcaccagcat taccacttat catactcctg attacaagtc ttaaattctcg 2940
 tgaagatata gcagtctggt tattatcaga aacagcagta cttgtactac taaccttttt 3000
 agaatatgaa aattgtgcac aagaatctga tggtttacca gttgtatcat cttgaccaac 3060
 taggaaacta tggttcagatg atataatccc ttccaaacct ttatatgatg tatctgaaat 3120
 agtatctcgc atattaatac cacgaatagc aaggctcactc atatcacaac cagtagactt 3180
 agtatcttca tgcttagata aattttctcaa caagccagta tcagcacttg caaacacaaa 3240
 atcgttctgt ttatcaggcc gaacaataaa gtcattocca cctaaactat ggttaagttt 3300
 tccaagactg ccatgaaatc caacttctat cctatattgt tgagagaaaag tagatctatc 3360
 caataatcca ccaacaccaa taaaactatc actagcatac tgcccaactc ttggattatc 3420
 acccatacaa aaactatccg gaaaaaact acgctttgga gacaaataac tattgaaatg 3480
 ttcaacttct gataataagt tagttgtgga ataagagcgc tttttttgaa caccaccttc 3540
 actatcatac tgatttaata ttctataagg tctatcccat ctctgtatac catcactaaa 3600
 aggtttaccc cattcttcta tatcgccact aaaaaattta tcccattttt ctataccacc 3660
 actaaaaggt ttactccatc tttcgagact attaccagta agaacaccat cttcttgtaa 3720
 tcttttatca ctttgtccgt tatatagaaa ttgatcacca catttagatt ctacatcctc 3780
 catctccatg tacgtcatat catctacacc ctcaggggaa ctttcactat cttgatcact 3840
 tgaattaaca ttttcatcat cagaagaacc cactacacca gcacaatctt ttcgttcttg 3900

tgattcctca ctaggtatag ttttagaact tactgaagaa gcctcagatt ccccatccag 3960
 attactatatt gttaaagtat ttcttccttc tcttccatag attttcttac aacaatacac 4020
 tatacaacta gcaattacga gcataataat gaacaccgta aatacaataa gcatttagcat 4080
 tcttatattc atattttaata cttctttata gattatcatt aataatatat aatttttttaa 4140
 tataaacaag actattttaat aaaaatatac tattttaacg gagattttta tgataattct 4200
 taaaattata aatatatattc ataacatgta acaagttatt gatataaaaa ataaaataat 4260
 attaacctta ctaagttata ttctaaaata attaaaaata atcttaaaat ctattaataa 4320
 gtacttatat acaattatat aataccatta ctaaataaacc atacagatc 4369

<210> 46
 <211> 1147
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(1147)
 <223> Complement to SEQ ID NO:45, nucleotides <1..1147
 Product = "14hworfli"

<400> 46
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<210> 47
 <211> 2766
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> misc_feature
 <222> (1)..(2766)
 <223> Complement to SEQ ID NO:45, nucleotides 1354..4119
 Hypothetical lipoprotein
 Product = "14hworf2"

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<210> 48

<211> 3500

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 48

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 gtattagata aagatagatc 3500

<210> 49
 <211> 753
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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 <222> (1)..(753)
 <223> Corresponds to SEQ ID NO:48, nucleotides 511..1263
 Hypothetical outer membrane protein
 Product = "18hworf1"

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 Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser
 20 25 30
 act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata 144
 Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
 35 40 45

acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca 192
 Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
 50 55 60

caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct 240
 Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
 65 70 75 80

gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa 288
 Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
 85 90 95

att gca ttt att gag ttc ttc gat tac tct tgt ggt tat tgt aaa atg 336
 Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
 100 105 110

atg ttt gaa gat atc aaa caa att ata aaa gat ggt aag gta cgt gtt 384
 Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
 115 120 125

att ttt aga gat ttt cca ata ctt ggg gaa tcg tcg tta aag gct gtt 432
 Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val
 130 135 140

aaa gca gca ttg gct gta cat ctt atc aat cca agt aaa tac ttg gac 480
 Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
 145 150 155 160

ttc tat tat gca gca tta aat cat aaa cag cca ttt aat gat gaa tct 528
 Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
 165 170 175

ata ctt aat ata gtt aaa tca ctt gaa att tca gaa gag gaa ttt aaa 576
 Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys
 180 185 190

gat tct tta tct aaa aat tct agt act att gat aag atg ata gag tcc 624
 Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser
 195 200 205

act aga aat ctg gct gag aag tta aat atc aga ggt act cct gct ctt 672
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 210 215 220

ata ata ggt gat gca ttc att ggg gga gct gca gat tta tca act tta 720
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<210> 50

<211> 250
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 50

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Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
 35 40 45

Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
 50 55 60

Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
 65 70 75 80

Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
 85 90 95

Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
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Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
 115 120 125

Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val
 130 135 140

Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
 145 150 155 160

Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
 165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys
 180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser

195

200

205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu
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Arg Ser Lys Ile Val Glu Gln Gln Glu Gln
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<210> 51
 <211> 2226
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <223> Complement to SEQ ID NO:48, nucleotides 1275..>3500
 Product = "18hworf2i"

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<211> 4750

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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<210> 53
<211> 371
<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(371)

<223> Complement to SEQ ID NO:52, nucleotides <1..371
Hypothetical integrase/recombinase
Product = "19hworfli"

<400> 53

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ctcaaatctc caattttaac atgcacaaga ttatttaatg taacagaaca ccctgtactc      240
ttatgcaaga actctataaa cttatcaagg tctcttacat aagaaacaac tgtattcaaa      300
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<210> 54

<211> 984

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(984)

<223> Corresponds to SEQ ID NO:52, nucleotides 632..1615
Hypothetical glycerol 3-phosphate dehydrogenase
Product = "19hworf2"

<400> 54

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att gca ctg tca gca cat ggt ata tca gtt aac tta tgg gga cgt gat      96
Ile Ala Leu Ser Ala His Gly Ile Ser Val Asn Leu Trp Gly Arg Asp
20          25          30

cat aga aat att aca cat ata aac act tac cga aaa aat tta aaa tat      144
His Arg Asn Ile Thr His Ile Asn Thr Tyr Arg Lys Asn Leu Lys Tyr
35          40          45

tta ccc aca tat cat cta cca gac aac ata tat gca acc agc aat ata      192
Leu Pro Thr Tyr His Leu Pro Asp Asn Ile Tyr Ala Thr Ser Asn Ile
50          55          60

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gac gaa gta tta tct gac aac aat aca tgt att atc tta act att cct 240
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 65 70 75 80

aca caa caa tta cgc acc ata tgt aca caa ata caa cac aaa cag cat 288
 Thr Gln Gln Leu Arg Thr Ile Cys Thr Gln Ile Gln His Lys Gln His
 85 90 95

atg tgt aaa aat act cca ata tta att tgt agt aaa ggt atc gaa att 336
 Met Cys Lys Asn Thr Pro Ile Leu Ile Cys Ser Lys Gly Ile Glu Ile
 100 105 110

aca tca ctc aaa ttt ccc agt gaa ata gca gaa gaa att tta caa tat 384
 Thr Ser Leu Lys Phe Pro Ser Glu Ile Ala Glu Glu Ile Leu Gln Tyr
 115 120 125

aat cca att ttt ata ctc tct ggt cca agt ttt gct aaa gaa att gca 432
 Asn Pro Ile Phe Ile Leu Ser Gly Pro Ser Phe Ala Lys Glu Ile Ala
 130 135 140

gaa cat ctt cct tgt agt ata gta ctt gct ggt gat aat aaa gaa ctt 480
 Glu His Leu Pro Cys Ser Ile Val Leu Ala Gly Asp Asn Lys Glu Leu
 145 150 155 160

ggt gaa tca ttg ata gaa aca ata agt aat gat gtt cta aaa ata ata 528
 Gly Glu Ser Leu Ile Glu Thr Ile Ser Asn Asp Val Leu Lys Ile Ile
 165 170 175

tac cat caa gat att ata ggt gta cag att gga gct gca tta aag aac 576
 Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn
 180 185 190

ata att gca att gca tgt gga ata atc gct gga aaa aat tta ggt aat 624
 Ile Ile Ala Ile Ala Cys Gly Ile Ile Ala Gly Lys Asn Leu Gly Asn
 195 200 205

aat gct gtt gct act gtt ata act aaa ggc atg aat gaa att aaa aca 672
 Asn Ala Val Ala Thr Val Ile Thr Lys Gly Met Asn Glu Ile Lys Thr
 210 215 220

cta tat ata gca aaa aat cat tca ata gat ctt cat aca tta att ggt 720
 Leu Tyr Ile Ala Lys Asn His Ser Ile Asp Leu His Thr Leu Ile Gly
 225 230 235 240

cca tca tgt ctt gga gat cta ata tta aca tgt aca aca gaa cat tca 768
 Pro Ser Cys Leu Gly Asp Leu Ile Leu Thr Cys Thr Thr Glu His Ser
 245 250 255

cgc aat atg gct ttt gga cta gaa ata gga aaa ggt aga aat ata aat 816
 Arg Asn Met Ala Phe Gly Leu Glu Ile Gly Lys Gly Arg Asn Ile Asn
 260 265 270

aca tta ata gat cac aac cta aag ctt gtt gaa gga acc agt act gta 864
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Cys Ile Ser Ile Tyr Asn Leu Leu His	Glu Asn Ile Ser Leu Asp	Lys	
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gcc ata tca aac ata tta tct tag			984
Ala Ile Ser Asn Ile Leu Ser			
325			

<210> 55

<211> 327

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 55

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Leu Pro Thr Tyr His Leu Pro Asp Asn Ile Tyr Ala Thr Ser Asn Ile	
50	55 60

Asp Glu Val Leu Ser Asp Asn Asn Thr Cys Ile Ile Leu Thr Ile Pro	
65	70 75 80

Thr Gln Gln Leu Arg Thr Ile Cys Thr Gln Ile Gln His Lys Gln His	
85	90 95

Met Cys Lys Asn Thr Pro Ile Leu Ile Cys Ser Lys Gly Ile Glu Ile	
100	105 110

Thr Ser Leu Lys Phe Pro Ser Glu Ile Ala Glu Glu Ile Leu Gln Tyr	
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Asn Pro Ile Phe Ile Leu Ser Gly Pro Ser Phe Ala Lys Glu Ile Ala	
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130

135

140

Glu His Leu Pro Cys Ser Ile Val Leu Ala Gly Asp Asn Lys Glu Leu
145 150 155 160

Gly Glu Ser Leu Ile Glu Thr Ile Ser Asn Asp Val Leu Lys Ile Ile
165 170 175

Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn
180 185 190

Ile Ile Ala Ile Ala Cys Gly Ile Ile Ala Gly Lys Asn Leu Gly Asn
195 200 205

Asn Ala Val Ala Thr Val Ile Thr Lys Gly Met Asn Glu Ile Lys Thr
210 215 220

Leu Tyr Ile Ala Lys Asn His Ser Ile Asp Leu His Thr Leu Ile Gly
225 230 235 240

Pro Ser Cys Leu Gly Asp Leu Ile Leu Thr Cys Thr Thr Glu His Ser
245 250 255

Arg Asn Met Ala Phe Gly Leu Glu Ile Gly Lys Gly Arg Asn Ile Asn
260 265 270

Thr Leu Ile Asp His Asn Leu Lys Leu Val Glu Gly Thr Ser Thr Val
275 280 285

Lys Pro Leu Ile Ser Leu Ala Lys Lys Leu Asn Val Glu Leu Pro Ile
290 295 300

Cys Ile Ser Ile Tyr Asn Leu Leu His Glu Asn Ile Ser Leu Asp Lys
305 310 315 320

Ala Ile Ser Asn Ile Leu Ser
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<210> 56

<211> 1416

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
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 <222> (1)..(1416)
 <223> Complement to SEQ ID NO:52, nucleotides 2467..3882
 Hypothetical nitrogen assimilation regulatory protein
 Product = "19hworf3"

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1416

<210> 57

<211> 597

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(597)

<223> Complement to SEQ ID NO:52, nucleotides 4154..>4750

Hypothetical cell division protein ftsQ

Product = "19hworf4i"

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aggtaat tttt atatttaaac cactagacaa aataatatcc caccaatgac tatcaacata 180

tgtgatagat gaaaccatac caccaacaag agtattatca ttgactactt cacgtataaa 240

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aggcacaaaa aagatagacc ttgcatcaac aagtttacgt atttcatcag aacttacata 540

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<210> 58

<211> 4544

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 58

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 agtccaaaa gattttgaag tactactact ttgtacttca tgcttaaaaag atcctgaaga 4200
 aaaactcata tcagttttta ctcgttgctc agtatcacac acattaaatt gcatatcaca 4260
 ttcagtatca caaaaagtac catttttaca tgatttcata catttttgct tcttatcctc 4320
 acatggatta ttactatctt ctttatcatc attaccttta ctgatagtat tgtttattat 4380
 actaataaat ggattacgac gagtttgctc atcaatcatt ttctctgcta atcgacaatc 4440
 tgtaactta acctgacatt gcctatagca atcattctta ttgtaactac attgaagtat 4500
 acatgctttg ccaacttcat tgtctggagc ttcatagttt gatc 4544

<210> 59

<211> 1566

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(1566)

<223> Corresponds to SEQ ID NO:58, nucleotides <1..1566
 Hypothetical phosphoribosylformylglycinamide synthase
 Product = "21hworfli"

<400> 59

gat cca att aca caa aag aaa ttg tct gat gct atc att aaa gaa gca 48
 Asp Pro Ile Thr Gln Lys Lys Leu Ser Asp Ala Ile Ile Lys Glu Ala
 1 5 10 15

aga gat tta aac tta tat aat gca atc act gat aat gga gcc gga ggt 96
 Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly
 20 25 30

cta tca tct tct ata ggt gaa atg gga aat aat gga ttt aaa gta gaa 144
 Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu
 35 40 45

cta aat aaa gta tta tta aaa cat aaa aac atg cta cct tgg gaa att 192
 Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile
 50 55 60

tgg gta tca gaa tca caa gaa aga atg aca tta gct att cct cca agc 240
 Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser
 65 70 75 80

aaa ttc cca ata ttt gaa aaa att atg aaa aag cat gat gtt gaa atc 288
 Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile
 85 90 95

agt att att gga aca ttc aat aat aca aaa aaa gca gta gta tca tat 336
 Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr
 100 105 110

aat gac tcc att att atg gat atg gat ata aac ttc tta cat aac ggt 384
 Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly
 115 120 125

ata cca aaa act cat cta aaa acc ata cca tgg tca aac ata ata tcc 432
 Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser
 130 135 140

tca gta gta gac aca tta cat aat aaa cca cta gac act gag cta aat 480
 Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn
 145 150 155 160

gaa atg atg caa aga atg aat ata tgt agt aaa gaa ttt atc tct aca 528
 Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr
 165 170 175

caa tat gat cat gaa gta cag gga aca tca gtc ata aaa cct ata caa 576
 Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln
 180 185 190

ggg aaa gga cga gta gat gga gaa gca ata gtt att aga cca ata cta 624
 Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu
 195 200 205

tca tca gaa agg gga cta gta aaa tca cat gga cta gga tca agc tat 672
 Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr
 210 215 220

gga gaa att agt aca tac cac atg gct gca tgt gct ata gat aca gca 720
 Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala
 225 230 235 240

ata cgt aat tat ata gca atc ggg gga aat ttc cat cac tta gca tta 768
 Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu
 245 250 255

tta gat aat ttc tgt tgg tgt gac tct aca aat cca aaa aga tta tgg Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp 260 265 270	816
caa tta aaa aat gct gcc caa gca tgt tat gaa tac gca aaa att ttc Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe 275 280 285	864
aaa aca cct ttc att tct gga aaa gat agc atg ttc aat gat ttt aaa Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys 290 295 300	912
ggg tat aac aat aaa gga gaa cct att aac att tct gct cct cct tca Gly Tyr Asn Asn Lys Gly Glu Pro Ile Asn Ile Ser Ala Pro Pro Ser 305 310 315 320	960
ctt tta att tct aca gta gga ata ata gaa aat att cac aat gcc ata Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile 325 330 335	1008
aca ctt gat gta aaa aat cca gga gat tta ata tac ata tta ggt gtg Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val 340 345 350	1056
aca tat gat gaa ctt gga agg tcc gaa tac caa aaa tat agc gga tta Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu 355 360 365	1104
gga aat aat aat gtt cca caa gta cgt gct aaa cat gca aaa aaa cta Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu 370 375 380	1152
tac aag tta tat agc aat gca gtt aat aca aat att ata gca tct gca Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala 385 390 395 400	1200
att gca tta aac cta ggg ggg cta att ata ggt tta ata aaa tca cta Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu 405 410 415	1248
att gga gga gaa ctg gga gca aaa att gac tta tca cta gta cca aca Ile Gly Gly Glu Leu Gly Ala Lys Ile Asp Leu Ser Leu Val Pro Thr 420 425 430	1296
cat aat att gaa gat aat aac ata aaa gag aaa gta atc cta ttt tca His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser 435 440 445	1344
gaa tca caa agt aga att tta gta aca ata gct cca cat aat aaa caa Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln 450 455 460	1392
aaa ttt gaa act att ttt aaa gac ata gca cat gca aac ata ggt ata Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile	1440

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<210> 60
<211> 521
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<400> 60
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Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly
20 25 30

Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu
35 40 45

Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile
50 55 60

Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser
65 70 75 80

Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile
85 90 95

Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr
100 105 110

Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly
115 120 125

Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser

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130

135

140

Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn
145 150 155 160

Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr
165 170 175

Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln
180 185 190

Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu
195 200 205

Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr
210 215 220

Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala
225 230 235 240

Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu
245 250 255

Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp
260 265 270

Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe
275 280 285

Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys
290 295 300

Gly Tyr Asn Asn Lys Gly Glu Pro Ile Asn Ile Ser Ala Pro Pro Ser
305 310 315 320

Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile
325 330 335

Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val
340 345 350

Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu
355 360 365

Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu
370 375 380

Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala
385 390 395 400

Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu
405 410 415

Ile Gly Gly Glu Leu Gly Ala Lys Ile Asp Leu Ser Leu Val Pro Thr
420 425 430

His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser
435 440 445

Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln
450 455 460

Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile
465 470 475 480

Ile Ser Asp Thr Asn Thr Leu Ile Ile Asn Asn Met His Ile Ile Asn
485 490 495

Leu Asn Thr Leu Lys His Ser Tyr Lys Lys Phe Ser Asn Met Lys Ile
500 505 510

Gln Ala Tyr Ala Asp Ala Glu Tyr Ile
515 520

- <210> 61
 <211> 525
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(525)
 <223> Corresponds to SEQ ID NO:58, nucleotides 2252..2776
 Hypothetical folic acid synthesis protein
 Product = "21hworf2"

<400> 61
 atg gct tac tca cct gac aat gat ata gta gta cta gca tta ggt agt 48
 Met Ala Tyr Ser Pro Asp Asn Asp Ile Val Val Leu Ala Leu Gly Ser
 1 5 10 15

 aat tgt ggc agt atg tta ttg aat att aaa tct gct ata aat atg tta 96
 Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu
 20 25 30

 tct tta tat aac aaa aca tat tct tat atc tat aaa agt atg gca cta 144
 Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu
 35 40 45

 tta cca gaa aat tct agt agt gat tgg gat act cct ttt ctg aat atg 192
 Leu Pro Glu Asn Ser Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met
 50 55 60

 gta gta tca ggt tat aca aat ctt tca cca aat ctt atg tta gaa aga 240
 Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg
 65 70 75 80

 gtt aaa tac att gaa aaa aaa ata ggc agg ttt aat aat gaa tac tgg 288
 Val Lys Tyr Ile Glu Lys Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp
 85 90 95

 tca cct aga tgt ata gat att gac att atc tta tgg gga gat aaa gtc 336
 Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val
 100 105 110

 tta gac tca caa act tta tct att cct cat aag cat atg caa gat aga 384
 Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg
 115 120 125

 gat ttt gta ctt gta cca ctc tgt gat att cac gca aga ttt cct cat 432
 Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His
 130 135 140

 cca gta tca aag cta tca att gaagaa ata gtt ctc aat cta cat gag 480
 Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu
 145 150 155 160

 atc aat tta ata aag cag tca tat att ata act caa tat tta tag 525
 Ile Asn Leu Ile Lys Gln Ser Tyr Ile Ile Thr Gln Tyr Leu
 165 170

<210> 62

<211> 174

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 62

Met Ala Tyr Ser Pro Asp Asn Asp Ile Val Val Leu Ala Leu Gly Ser
1 5 10 15

Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu
20 25 30

Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu
35 40 45

Leu Pro Glu Asn Ser Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met
50 55 60

Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg
65 70 75 80

Val Lys Tyr Ile Glu Lys Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp
85 90 95

Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val
100 105 110

Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg
115 120 125

Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His
130 135 140

Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu
145 150 155 160

Ile Asn Leu Ile Lys Gln Ser Tyr Ile Ile Thr Gln Tyr Leu
165 170

<210> 63

<211> 560

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(560)

<223> Complement to SEQ ID NO:58, nucleotides 3985...>4544

Product = "21hworf3i"

<400> 63

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agtaaaacat aaatcataat cactcctaca taatctatca caatcattta ccttacataa	120
acttacaggt ttcacaggaa ctacagattt tataccagct ccaaaagatt ttgaagtact	180
actactttgt acttcatgct taaaagatcc tgaagaaaaa ctcatatcag ttttaactcg	240
ttgctcagta tcacacacat taaattgcat atcacattca gtatcacaaa aagtaccatt	300
tttcatgat ttcatacatt tttgtctctt atcctcacat ggattattac tatcttcttt	360
atcatcatta cctttactga tagtattggt tattatacta ataaatggat tacgacgagt	420
ttgtgcatca atcattttct ctgctaactg acaatctgtt aacttaacct gacattgcct	480
atagcaatca ttcttattgt aactacattg aagtatacat gctttgccaa cttcattgtc	540
tggagcttca tagtttgatc	560

<210> 64

<211> 4483

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 64

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ctagaatttc actaagaata tctgcaccag ttattttcact tataccagaa ctatgagcat	180
gtataatagc tctatgaact aacctttcaa aaataatagt aggcttaact tctgagatac	240
ctttatcaat tagagtaggt atttcatatc ttaaaaaatt tataatagta attttttagct	300
tatcaataga tacacgaaat gcataaaaaa cacgtctagc atctatatca tccgttaacg	360
ccaataaaag atgttctaaa gtagcatatt catgatgaaa atcaaacgca attgataatg	420
ccttatgcaa actatcttca agattctttg ataacactaa tgtccctaatt ctatattttc	480
agacactcta tctactgaaaa attaaaaata agttgcaaata gataatacat caatttcata	540
atcaatactg tgcaataaat ttttaatat gtacttataa aaaacatatg ttacacaatg	600
atgcttaaac taactactta tatatgtttg aaaacgatat attcaagttt ttcacactac	660
tactattaga aatcatttta ggtatagata atgtgatttt tatatcactt gccgttataa	720
aagtaccaga taccttacgc aacaaagtaa gatatatagg actagcatta gcattaataa	780

tgcgactcgt tgcattacag acagcatoga tattattgtc actaaataaa ccagtaatat	840
tcctagcaca acttcattta tcaccaata acttatttat gatatttgga ggagtattct	900
taatatatca cagcatatgt gaaatattgg atgatatttc aaaaaagct catgataaga	960
atcttcataa cttaaaatca aacccttact tagtaatact acagataata ttaatagact	1020
tagtattctc aatagattca atactcactg ctataggaat tacatataac atttttataa	1080
tccaactagt atttataata tccataatac ttacaatctt attttcaaag catatcatag	1140
aagctattac aaaatacagt aacatcaaaa ctatagctgt catgtttgtc ttaatattag	1200
gtatcatact agtactagat ggaatacata ttaaaatata ccataattat ttatatttta	1260
cctttatctt ttctagcctc gttgaaataa taaatattat aaaaaagtca agcaatagcc	1320
taatacagta aaattaataa gcataatagg taatttattt aattcattat acaatgatat	1380
ctctaaaaat ttatacacia attgtaaaga gacacatata acataaatta aaatatgtta	1440
tatataccgt aatcattcac aggattatat ttaatcacia tagatattac tacgtacaac	1500
aattagctct aatattttac tttaaattt acaattaata ttgttaccac tataattata	1560
ttactaaaaat taaaattttg ttttgttgt aattttgatt ttaagtattt ttatttagatg	1620
tttaaagagt attgacaata ttacttattt actttaaaaa aaagggtttt gacaattttt	1680
agtttctaag tagacatcaa tatgtctaaa acagaaatgg aatataaatc tttttttata	1740
caaagaatac tacaactata gtggaatgt cagtttacat tgctaaagat tgttattttt	1800
acaattaaat gcctttaatt atatatatta ccgtatatgg ttattattat ttacagtat	1860
acaaattctt tacacataaa aattttaaag ttttttgta ttatttatta ataaactaat	1920
agaagtacaa tatattctgt atttaacttc ttttaaattt gatattctaa taaattgata	1980
aaagtatatt atacttaaac tttgtgatac atatcctttg cctaattata aaaaatgatt	2040
ttttattgaa atagttaata tgttattcaa aatatttgaa taacatgtaa gaatgattgt	2100
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ataaatctac acaatacata ctactgtatt tattaaatga acatatataa caaattactg	2280
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cacagttact gcttgattac tattgattac ttttttgta caatacacat aacattttac	2400
taattaactg ataactctag cgttgcgaaa ttatcataaa tatcattatt taatataaca	2460

agaataacac ataataatat taacaatgta cactagaaat aataactaac aagatataaa 2520
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 tattacctac agaaaacact ttctcacag acaaagtacc tatctgtacc tcttgtttca 3180
 atggcctcaa cataccagtt agtatcttct taatatcatc tattatatcg tatataacaa 3240
 aataatgctt tatttcgata tttttctggt ttgccaattc ttttacttgc gtatccgttt 3300
 taacattaaa tgctaaaatt attgaatttg atgtttccgc taataaaaca tctgactttg 3360
 taatattccc tacaccttta tatagaatat taactcgtat atctttatga gtaattttac 3420
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 ctacaacaat aaaactagta ccaaaatttg ggacattatt taaaccaaata accttaattg 3660
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 taccataage ttgattacct gcaacaataa tatcaccaac tttcaaggta cctttttgta 3780
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 attttaactg atctaagttt attttctctt ttgctgatac aggaacaaca ataacatcac 3960
 ctctaaact ttctgtacc actccatgct gtaataaage attagtaatt ctatctaaat 4020
 cagcatcatg tttatcaatt ttattaaccg caactatcat agcaacatta gctgccttta 4080

catgattaat agattcaata gtttgtggca taataccatc atcagcggcc actactagca 4140
 ctactatatac agtaacatta gtacatgag ctctcatagc agcaaatgct tcatgtcctg 4200
 gtgtatcaat aaaagttatc ttcttatctc cattcaatgt gatctggtac gcacctatat 4260
 gttgtgttat ccctttaaat tccccatcaa caacgtttga ttcacgtata gcatcaagca 4320
 atgaagtttt tccatgatca acatgtccca taacagtaac aactggtgct ctaggaatca 4380
 attccatatt attacatca gaataataat cattttctaa tttagcattg tctaccaact 4440
 taaatgtatg attgaacgct tctactataa tagaagcttg atc 4483

<210> 65
 <211> 708
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(708)
 <223> Corresponds to SEQ ID NO:64, nucleotides 624..1331
 Hypothetical transmembrane protein
 Product = "23hworf1"

<400> 65
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 Met Phe Glu Asn Asp Ile Phe Lys Phe Phe Thr Leu Leu Leu Leu Glu
 1 5 10 15
 atc att tta ggt ata gat aat gtg att ttt ata tca ctt gcc gtt ata 96
 Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile
 20 25 30
 aaa gta cca gat acc tta cgc aac aaa gta aga tat ata gga cta gca 144
 Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala
 35 40 45
 tta gca tta ata atg cga ctc gtt gca tta cag aca gca tcg ata tta 192
 Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu
 50 55 60
 ttg tca cta aat aaa cca gta ata ttc cta gca caa ctt cat tta tca 240
 Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser
 65 70 75 80
 ccc aat aac tta ttt atg ata ttt gga gga gta ttc tta ata tat cac 288
 Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His
 85 90 95
 agc ata tgt gaa ata ttg gat gat att tca aaa aaa gct cat gat aag 336
 Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys

100	105	110	
aat ctt cat aac tta aaa tca aac cct tac tta gta ata cta cag ata			384
Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile			
115	120	125	
ata tta ata gac tta gta ttc tca ata gat tca ata ctc act gct ata			432
Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile			
130	135	140	
gga att aca tat aac att ttt ata atc caa cta gta ttt ata ata tcc			480
Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser			
145	150	155	160
ata ata ctt aca atc tta ttt tca aag cat atc ata gaa gct att aca			528
Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr			
165	170	175	
aaa tac agt aac atc aaa act ata gct gtc atg ttt gtc tta ata tta			576
Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu			
180	185	190	
ggt atc ata cta gta cta gat gga ata cat att aaa ata tcc cat aat			624
Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn			
195	200	205	
tat tta tat ttt acc ttt atc ttt tct agc ctc gtt gaa ata ata aat			672
Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn			
210	215	220	
att ata aaa aag tca agc aat agc cta ata cag taa			708
Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln			
225	230	235	

<210> 66

<211> 235

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 66

Met Phe Glu Asn Asp Ile Phe Lys Phe Phe Thr Leu Leu Leu Glu
1 5 10 15

Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile
20 25 30

Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala
35 40 45

Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu

50

55

60

Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser
65 70 75 80

Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His
85 90 95

Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys
100 105 110

Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile
115 120 125

Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile
130 135 140

Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser
145 150 155 160

Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr
165 170 175

Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu
180 185 190

Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn
195 200 205

Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn
210 215 220

Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln
225 230 235

<210> 67

<211> 348

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (1)..(348)

<223> Complement to SEQ ID NO:64, nucleotides 2526..2873
 Hypothetical ribosome-binding factor A
 Product = "23hworf2"

<400> 67
 ttatttagat tctaataatt ggtttactct tactaaatta tcaaaatgat aatcaatttt 60
 aaaatataat ttcggtacat atctaagatc tacatatgaa aatatagcct ttcttatttaa 120
 aatgaaaca tcgttttagtt cttttacaag attttcttta tctggatgat catcggaat 180
 tacaacaaat acagtagcat tttttacatc ttactcact tctacttttag atacattaac 240
 tatactacaa cctattgaat aaatatcatg tatcaatact ctcgatattg ctctgcttaa 300
 tactgaagca acctttaaat ttctaaaact ctcagattta taaatcat 348

<210> 68
 <211> 1614
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(1614)
 <223> Complement to SEQ ID NO:64, nucleotides 2870..>4483
 Hypothetical translation initiation factor IF-2
 Product = "23hworf3i"

<400> 68
 tcattgtata actctaattt cttctactat ctcaaatata ttcataacat cactttctgg 60
 atatattctt tttgaataat caagtaaaat accacattca aagccagcag taacttcctt 120
 tacatcatct ttaaactgac gtaagacttt aatcttacct tcatgcataa tattattatt 180
 acgaactaac ttaactaatg cacctttttt taccaaacca cttgttacat aacaccaag 240
 tacactaccg ttattaccta cagaaaacac ttttctcaca gacaaagtac ctatctgtac 300
 ctcttgtttc aatggcctca acataccagt tagtatcttc ttaatatcat ctattatatt 360
 gtatataaca aaataatgct ttatttcgat atttttctgt tttgccaatt cttttacttg 420
 cgtatccgtt ttaacattaa atgctaaaat tattgaattt gatgtttccg ctaataaaac 480
 atctgacttt gtaatatcc ctacaccttt atatagaata ttaactcgta tatctttatg 540
 agtaatttta ccaattgaat aacatatagc ttctatagaa ccataacat cacactttaa 600
 gataacgttc aactcatcaa ccatatcata aagcaatata ttactcttat cgattgctgg 660

ctgtttactc aattccacat ttagtaaate ttgcctataa ttaattaatt cacgtgcttg 720
 tttttcagaa tctacaacaa taaaactagt accaaaattht gggacattat ttaaaccacaa 780
 taccttaatt ggcattgaag gaatagcaac tttttcactc ccaccatctg cattaaacat 840
 actacgcacc ctaccataag cttgattacc tgcaacaata atatcaccaa ctttcaaggt 900
 acctttttgt actattaacg tagcaactac tccacaattc ttatcaactt ttgattcaat 960
 tactgtacca gatgccttag tattatatac agcttttaac tctaacaaat ctgcaatcaa 1020
 caatatactt gatttttaact gatctaagtt tttttctcc tttgctgata caggaacaaac 1080
 aataacatca cctcctaaac tttctgctac cactccatgc tgtaataaag cattagtaat 1140
 tctatctaaa tcagcatcat gtttatcaat tttattaacc gcaactatca tagcaacatt 1200
 agctgccttt acatgattaa tagattcaat agtttggtggc ataataccat catcagcggc 1260
 cactactagc actactatat cagtaacatt agtaccatga gctctcatag cagcaaagtc 1320
 ttcatgtcct ggtgtatcaa taaaagttat cttcttatct ccattcaatg tgatctggta 1380
 cgcacctata tgttggtgta tccctttaaa tccccatca acaacgtttg attcacgtat 1440
 agcatcaagc aatgaagttt ttccatgatc aacatgtccc ataacagtaa caactgggtgc 1500
 tctaggaate aattccatat tattaccatc agaataataa tcattttcta atttagcatt 1560
 gtctaccaac ttaaatgtat gattgaacgc ttctactata atagaagctt gatc 1614

<210> 69

<211> 3829

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 69

gatccagaaa attcagtgct attttcacag tcttttattc cagcacatac agagttacta 60
 tggatattca gttgcattac ttcaacaggt caactaaata gaatgactca atttaaagaa 120
 aaaagccgca ataaagtttc tacagcttct ttaggattgt acagctatcc tgtattaatg 180
 gcagctgata tattacttta ccaagcaaatt atagtacctg taggcattga tcaaaaaacaa 240
 cacttagaat tagcacgaga cattgctcaa gcttttaaca caaaatacaa tacgcaatac 300
 tttcaactgc cagaaccatt aattgtacag gaatcagcaa aaattatgag ttttaagagac 360
 ggtaaaaaga aaatgagtaa atctgatgta tcagattatt cacgaattaa tttagaagat 420
 agtaacgact taattgctca aaaaattaac aaagcaacca ctgactctat tgtaggtttt 480

gactttacaa gtttaaacia taggcctgca gtaaagaatc ttgttaatat ttatgctaca 540
 ctttcaaata ttagtataga acaaacatgt actaacattg caagcttcac tactaaacia 600
 tttaaagaag aactaacaga attaattatt aataacattg caccaatacg aaaaaatta 660
 agagagttat tagaagacat agaatatatta cgaagcatat taatgacagg aaataacaag 720
 gctgcatcta ttgcacataa gcacataata gaaattaaaa agattgcagg atattggtaa 780
 taattataca aaattcatta atactcaaag tcatatcctt tggttattat tgtatgtgtc 840
 atggtgttta aaaacataaa atagttttta ttaccaatat gtaaagatca aggaaattat 900
 tacaatatat taatatcaac agtctcagta tgttgagaga ttcatatatta ttttaattaaa 960
 ctataatctt cttgactatc atctttatat attaggccat tttatataaa aaaaaagaaa 1020
 agaaatccta ctcattaata tctaaatatt aaaagagcta ctacaaaata actaccataa 1080
 tacatctata gcaaaataaa gaatccatag catcaaaata tctatactaa attcactatc 1140
 catatctagt ccgcatctat aatactataa aattaacact gtataacaaa atatgtagtg 1200
 ttaatgccta taaaattaac aatattacta gaaaattaaa taccctaata taatactacc 1260
 aaagatatcc actaaataaa agtacaataa taataaacia aaagagacat agaggaatag 1320
 ttatatatta tatcagctac taactgttat aaacatatag cttaatatat atttactcaa 1380
 gtccataaaa tacacattct cacaagagtt agtacacagt aaagagaaaa aaaagtttagc 1440
 acttgaagag ttcacttacc aatatactat tcagtttcat taaaaaaatt acacaatttt 1500
 ttttctaaat ataattcaga atttactatt ctatatagtg attctattca cttaagcatt 1560
 atctatatac atagtatatc acaaactctca ctttaatatc cttttttacac actcatcaaa 1620
 tccaatactc ataataaaat aagttattta ttcaaaatac tattgaatat taacgaaaat 1680
 ctataggaca atataacatt agatgttatt aaccattttt ataataaaca gtatacactg 1740
 ttgtattact ttaacttcaa ttatagaaaa tgaaaaatag tatagaattt aaagttatta 1800
 ttaatgctct ataactctat ttatacccta gtgtaaaatc taaataatat ttttcttact 1860
 tatcaataaa aacaataaat attaccacat aacctaaagca tactcttcat aaacttaagt 1920
 aacaatatct cattatatatt atttttcaaa aataaactat aagcaattat taccatctaa 1980
 gcttatctaa atataattta tctatactat accattataa atctgattac tataaagatt 2040
 gaactatagt catccaaagg tttatacttg cttaatttta ctttacacia aacaacaatt 2100
 aaaaattata tataataaaa aatttactat tataaaaggc taacaaataa tcaactttac 2160

gtacatgagt aaattcctttc tgattatgct attttaataa taaaaaatac tatattttgt	2220
gagaaaaata tagtaataat atgctgtaat taacacacga aaggatttac ctctgtatt	2280
tataggagat aaatccttgt acagatacca caattaaata aaacaattaa ttcattctaa	2340
tattatttat atgggtttca ttagatgcca gtaaatactc tttcaccact acgaccacca	2400
aatgtaaadc cttttgctac ttctgggcta cttgttaca ctgacccctc tgggctactt	2460
gttacaactg atccttctgg gctacttggt acaactgac cttctgggct acttggtaca	2520
actgacccct ctgggctact tgttacaact gatccctctg ggctacttgt tacaactgat	2580
ccttctgggc tacttggtac aactgaccc tctgggctac ttgttacaac tgatccctct	2640
gggctacttg ttacaactga tccttctggg ctacttggtt caactgatcc ttctgggcta	2700
cttggtacaa ctgacccctc tgggctactt gttacaactg atccttctgg gctacttggt	2760
acaactgac cttctgggct acttggtaca actgacccct ctgggctact tgttacaact	2820
gatccctctg ggctacttgt tacaactgat ccttctgggc tacttggtac aactgaccc	2880
tctgggctac ttgttacaac tgatccctct gggctacttg ttacaactga tccttctggg	2940
ctacttggtt caactgatcc ttctgggcta cttgttacag ctgctccctc tgggctatct	3000
gttacagttg tatcaacacc tgagatcacc ttatcatagc acacatttaa tggatgaaga	3060
ttaagagaaa aattagaacc ttgttgtaaa aactctgaaa aagggtccat taaatttact	3120
acaaaagaag cttgtaagct gtgggtttaat acatcaagt caatatgttt accagtaaca	3180
ccatgaaaat ctgaaagtac gtgaccatta ctgtaaaaca taacatgata ttcgccatga	3240
tgattttcat gaccttcttc atgctcatga ggatgatagc caatctccat tgtaatatca	3300
ccatttgaaa cagagaattg attattacta tagatactta aatcatttcc aaaatcaata	3360
ttgtcaattc ttgttggtta atgaagcata caatcttctg ctgttgatg aaccatacag	3420
taacctatta gtacaatgca ttttatatt atatatttta gtgtgttaat tttgttttaa	3480
gtacaacttt gtgtagtaaa taagtcacac tacttttcaa tctctacaat tacgaagata	3540
cagatgtaaa ttcgctatct tgagaagccg tatcagtaac agatactaaa ttagcactta	3600
cacaatcaac attatgattg tggcaatctt ctgttaatgg atgaagatta agagaaaaat	3660
tagaaccttg ttgtaaaaac tctgaaaaag gttccattaa atttactaca aaagaagctt	3720
gtaagctgtg atttaataca tcaagtgcaa tatgttgacc agtaacacca tgaaaatctg	3780

aaagtacgtg accattatatt ataaacataa catgatattc cccatgatc

3829

<210> 70
 <211> 780
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(780)
 <223> Corresponds to SEQ ID NO:69, nucleotides <1..780
 Hypothetical tryptophanyl-tRNA ligase
 Product = "26hworfli"

<400> 70
 gat cca gaa aat tca gtg cta ttt tca cag tct ttt att cca gca cat 48
 Asp Pro Glu Asn Ser Val Leu Phe Ser Gln Ser Phe Ile Pro Ala His
 1 5 10 15
 aca gag tta cta tgg ata ttc agt tgc att act tca aca ggt caa cta 96
 Thr Glu Leu Leu Trp Ile Phe Ser Cys Ile Thr Ser Thr Gly Gln Leu
 20 25 30
 aat aga atg act caa ttt aaa gaa aaa agc cgc aat aaa gtt tct aca 144
 Asn Arg Met Thr Gln Phe Lys Glu Lys Ser Arg Asn Lys Val Ser Thr
 35 40 45
 gct tct tta gga ttg tac agc tat cct gta tta atg gca gct gat ata 192
 Ala Ser Leu Gly Leu Tyr Ser Tyr Pro Val Leu Met Ala Ala Asp Ile
 50 55 60
 tta ctt tac caa gca aat ata gta cct gta ggc att gat caa aaa caa 240
 Leu Leu Tyr Gln Ala Asn Ile Val Pro Val Gly Ile Asp Gln Lys Gln
 65 70 75 80
 cac tta gaa tta gca cga gac att gct caa gct ttt aac aca aaa tac 288
 His Leu Glu Leu Ala Arg Asp Ile Ala Gln Ala Phe Asn Thr Lys Tyr
 85 90 95
 aat acg caa tac ttt caa ctg cca gaa cca tta att gta cag gaa tca 336
 Asn Thr Gln Tyr Phe Gln Leu Pro Glu Pro Leu Ile Val Gln Glu Ser
 100 105 110
 gca aaa att atg agt tta aga gac ggt aaa aag aaa atg agt aaa tct 384
 Ala Lys Ile Met Ser Leu Arg Asp Gly Lys Lys Lys Met Ser Lys Ser
 115 120 125
 gat gta tca gat tat tca cga att aat tta gaa gat agt aac gac tta 432
 Asp Val Ser Asp Tyr Ser Arg Ile Asn Leu Glu Asp Ser Asn Asp Leu
 130 135 140
 att gct caa aaa att aac aaa gca acc act gac tct att gta ggt ttt 480
 Ile Ala Gln Lys Ile Asn Lys Ala Thr Thr Asp Ser Ile Val Gly Phe

145	150	155	160	
gac ttt aca agt tta aac aat agg cct gca gta aag aat ctt gtt aat				528
Asp Phe Thr Ser Leu Asn Asn Arg Pro Ala Val Lys Asn Leu Val Asn				
	165	170	175	
att tat gct aca ctt tca aat att agt ata gaa caa aca tgt act aac				576
Ile Tyr Ala Thr Leu Ser Asn Ile Ser Ile Glu Gln Thr Cys Thr Asn				
	180	185	190	
att gca agc ttc act act aaa caa ttt aaa gaa gaa cta aca gaa tta				624
Ile Ala Ser Phe Thr Thr Lys Gln Phe Lys Glu Glu Leu Thr Glu Leu				
	195	200	205	
att att aat aac att gca cca ata cga caa aaa tta aga gag tta tta				672
Ile Ile Asn Asn Ile Ala Pro Ile Arg Gln Lys Leu Arg Glu Leu Leu				
	210	215	220	
gaa gac ata gaa tat tta cga agc ata tta atg aca gga aat aac aag				720
Glu Asp Ile Glu Tyr Leu Arg Ser Ile Leu Met Thr Gly Asn Asn Lys				
	225	230	235	240
gct gca tct att gca cat aag cac ata ata gaa att aaa aag att gca				768
Ala Ala Ser Ile Ala His Lys His Ile Ile Glu Ile Lys Lys Ile Ala				
	245	250	255	
gga tat tgg taa				780
Gly Tyr Trp				

<210> 71
 <211> 259
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 71

Asp Pro Glu Asn Ser Val Leu Phe Ser Gln Ser Phe Ile Pro Ala His			
1	5	10	15
Thr Glu Leu Leu Trp Ile Phe Ser Cys Ile Thr Ser Thr Gly Gln Leu			
	20	25	30
Asn Arg Met Thr Gln Phe Lys Glu Lys Ser Arg Asn Lys Val Ser Thr			
	35	40	45
Ala Ser Leu Gly Leu Tyr Ser Tyr Pro Val Leu Met Ala Ala Asp Ile			
	50	55	60
Leu Leu Tyr Gln Ala Asn Ile Val Pro Val Gly Ile Asp Gln Lys Gln			

65

70

75

80

His Leu Glu Leu Ala Arg Asp Ile Ala Gln Ala Phe Asn Thr Lys Tyr
85 90 95

Asn Thr Gln Tyr Phe Gln Leu Pro Glu Pro Leu Ile Val Gln Glu Ser
100 105 110

Ala Lys Ile Met Ser Leu Arg Asp Gly Lys Lys Lys Met Ser Lys Ser
115 120 125

Asp Val Ser Asp Tyr Ser Arg Ile Asn Leu Glu Asp Ser Asn Asp Leu
130 135 140

Ile Ala Gln Lys Ile Asn Lys Ala Thr Thr Asp Ser Ile Val Gly Phe
145 150 155 160

Asp Phe Thr Ser Leu Asn Asn Arg Pro Ala Val Lys Asn Leu Val Asn
165 170 175

Ile Tyr Ala Thr Leu Ser Asn Ile Ser Ile Glu Gln Thr Cys Thr Asn
180 185 190

Ile Ala Ser Phe Thr Thr Lys Gln Phe Lys Glu Glu Leu Thr Glu Leu
195 200 205

Ile Ile Asn Asn Ile Ala Pro Ile Arg Gln Lys Leu Arg Glu Leu Leu
210 215 220

Glu Asp Ile Glu Tyr Leu Arg Ser Ile Leu Met Thr Gly Asn Asn Lys
225 230 235 240

Ala Ala Ser Ile Ala His Lys His Ile Ile Glu Ile Lys Lys Ile Ala
245 250 255

Gly Tyr Trp

<210> 72

<211> 1056

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(1056)
 <223> Complement to SEQ ID NO:69, nucleotides 2361..3416
 Similar to cell surface mucin, protein contains 9-mer tandem repe
 at
 Product = "26hworf2"

<400> 72
 ttagatgcc a gtaaatactc tttcaccact acgaccacca aatgtaaatac cttttgctac 60
 ttctgggcta cttgttaca ctgacccctc tgggctactt gttacaactg atccttctgg 120
 gctacttggt acaactgac cttctgggct acttggtaca actgacccct ctgggctact 180
 tgttacaact gatccctctg ggctacttgt tacaactgat ccttctgggc tacttggtac 240
 aactgaccc tctgggctac ttgttacaac tgatccctct gggctacttg ttacaactga 300
 tccttctggg ctacttggtt caactgatcc ttctgggcta cttgttaca ctgacccctc 360
 tgggctactt gttacaactg atccttctgg gctacttggt acaactgac cttctgggct 420
 acttggtaca actgacccct ctgggctact tgttacaact gatccctctg ggctacttgt 480
 tacaactgat ccttctgggc tacttggtac aactgaccc tctgggctac ttgttacaac 540
 tgatccctct gggctacttg ttacaactga tccttctggg ctacttggtt caactgatcc 600
 ttctgggcta cttgttacag ctgctccttc tgggctatct gttacagttg tatcaacacc 660
 tgagatcacc ttatcatagc acacatttaa tggatgaaga ttaagagaaa aattagaacc 720
 ttgttgtaaa aactctgaaa aagggtccat taaatttact acaaaagaag cttgtaagct 780
 gtggtttaat acatcaagtg caatatgttt accagtaaca ccatgaaaat ctgaaagtac 840
 gtgaccatta ctgtaaaaca taacatgata ttgccatga tgattttcat gaccttcttc 900
 atgctcatga ggatgatagc caatctccat tgtaatatca ccatttgaaa cagagaattg 960
 attattacta tagatactta aatcatttcc aaaatcaata ttgtcaattc ttgttggttaa 1020
 atgaagcata caatcttctg ctgttgaatg aaccat 1056

<210> 73
 <211> 300
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature

<222> (1)..(300)

<223> Complement to SEQ ID NO:69, nucleotides 3530...>3829

Similar to 26hworf2

Product = "26hworf3i"

<400> 73

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attagcactt acacaatcaa cattatgatt gtggcaatct tctgttaatg gatgaagatt 120

aagagaaaaa ttagaacctt gttgtaaaaa ctctgaaaaa ggttccatta aatttactac 180

aaaagaagct tgtaagctgt gatttaatac atcaagtgc aatgttgac cagtaacacc 240

atgaaaatct gaaagtacgt gaccattatt tataaacata acatgatatt ccccatgatc 300

<210> 74

<211> 4460

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 74

gatcaattat tagttgcttc tgtagttgat tgtatggaat attttgctaa cttagtcaat 60

aagcgatta ctagtaaagt gaaacgttat atttctatat taagtacttc tatatatgac 120

gtgtctgttg ttgagttatt taatcggcgt aacaatataa tagatagaat gttgtgctaa 180

aaggatattt tatatttgtg taaaaggatt ttattaatag gggtcctaata taacattggg 240

gaattaaaac atatttttaa taaattcttt atatgtgtag tacatagtga aatagtaa 300

cttgtgttg tataaattca tactttttca ctttcaattt aataacgtca ttttctggat 360

aaatagttat gaaactttct ttgtatatag ttagtactat aggtgtgatt atattgttac 420

tttgcttgat gttaattttg tattgtatcg atattgcata tgctaataatt aaaaactgtg 480

ttttcaataa tactgataaa actaaaaatg ctgtgaattt atctattgaa aacaggggta 540

aaaactctgt tttatgtggg ctaaaaaaag aatttagaag tacattaaga aatttttgtg 600

attataacaa tgtaactct gtagaagcaa aatctgctca atatggtagt ctgatggtaa 660

aagctgggtc taaatacatc caagatttaa tatctgaaat agatgaccga attgttaatc 720

agtatattac tgggagggta ttatcactag aagtattaat aatgcaattt gaggatacaa 780

tatatactat atgtaatgag gaaactatac agtgcgaact acaaagagtg ctatatgtac 840

gtttgctttt aaataatatt ttaaagttga caaaaagtat atgtgaacaa agtgatattg 900

aattaatgga aatatatgga atgaaatttg aatatgcttt atcttttatt catagtgggt 960

ttacttatat aatgaaaaat atatgtacat taagtggtaa tgtttattgt aataatcaaa 1020
 aacagttgtg tactgatgat gttactttta ctactatatac attatatgat ataaaccatt 1080
 gtattagtca ttagataaat ttctaagctt tatttgtatt tgttatgtgg aatgttcaaa 1140
 tattaggtta attttattca cttagataag tagtgtctat tgggtataaat taacttgtgc 1200
 tttttattct ataaattgta atagtgtatg tctaatacgt taattcttaa ctatcttggg 1260
 cagtgttgaa ttattttatt tgctaatttt tactgatgtg aaaagtaaatt attgatatgt 1320
 aagttatgta atattattta attactaatt tcagttatgt tgcattagta tgacataact 1380
 gtatatttaa aattatgtat tagtataaatt ttattcaaca gttttgttaa actaagatgt 1440
 aatttagttt gttgtaagt tagtatttca atttttaatt tttgatatat taatgttagc 1500
 taggtaatat ataatttgta tatttgatat acaaaatatt agtactattg attatataca 1560
 tgatcaaatt tgttataatt gtaaggggaaac taaatgagag tttcatttat gtagagaata 1620
 tgattagtgt tttattgtag tcaatatattc ttgacatttt tactagttat attttttatt 1680
 gtttgtgata cggttaataca agatattaga aaatatatat agactactaa ttagcttatac 1740
 aaaaaataaa gttttatata tttaaacttag tattaagaa ataaagaatt ataacctgat 1800
 atgttaagtt atgtgataag gtaacggatt taacaagagc tgtttttttt aacttttatg 1860
 ttatattaat gtattattta tatgtacata ttatggatca attggtgtat ataaattagg 1920
 atgatagatc tcaagtatct ttttatattt tgtaattta tattagtttg atcttcatgc 1980
 taacatcagt actagttatt ttagagaagt agtattaaag tacagggttg tatagtttat 2040
 ttttaatttt tagctgttca tattgagtta acataaatgt ttaagtatgt tatggcttat 2100
 ggaattatta aagagtatta agcttagaat tttcaatttt attgtttatt aagttagtgt 2160
 aggtactagt ttggtgtcaa tgtattgtag tgaagtaacg tcaggaatta caaatctcca 2220
 gaatttatct gttgccttac taatgcctat tctgggggtg caaatataat catctatatt 2280
 gagatttgta ttacaaatgc agaaactatg atttgctgtc atgtctatat tgttatgttc 2340
 ttttgttatg tgtaggggtt tacatatattt tcttgggtcca ttaacttttg tatgtgggtg 2400
 atttttagat aataagatta tacttcgaat taatattgct gcagggaaac cttcagggtc 2460
 tgtaacaacg ttgaggcagt gatacattcc atagattaaa taaacataag agaattccagg 2520
 gttaccaaac attacagcag tgcgctttgt atatccgtgg aaagaatgtg ctgcttgatc 2580

atcttgcct atatatgctt ctgtttctgt tataatccct ttgtgttgat taaaaagtaa 2640
 catcttgcct agtaagctgc ttgcaacatc aagtgatttt tgtttataaa atgacttctt 2700
 taatatgttg tacatgtatt gtctttatca ctactatggg actattttaca actaattata 2760
 ttagtgatgt ataatttttg tcaattaatg gaaatgagct atggatagtg tgaagaaggg 2820
 gtagatattt tgttaatata aaaaagctat gtgcattata atagaatacg aaatgtattt 2880
 tacaaaatta cttttattat tggtgatata taagtatagg tttaagaata tgcatagctt 2940
 ttcaatatta aagtaagata ctataggtag aattagttag cgtataaaat attaattgcta 3000
 tagaaggata aattgattaa ggaatatatt tagtatataa gtaacgtgac tatccatatt 3060
 tagttatatt ataattgtaa taattatgaa agtattgttt aatgttatct aaattataat 3120
 gtttttaagt tttcaagtag agttagtaat ttgttggaag catataatat tcataagtta 3180
 ttttttagtg ctagttatat gatatgtgta ctttgtaaga gaactttagt aacattattt 3240
 aattagggta aattgattta ttagcattat aaagattttt ataaattgta caactattcc 3300
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 gttactgatt aatgggtgtg tatgccgtat agagattttg ctataacttg gttagctata 3420
 ttgatagcgt gtatcatcac gatatgtgta ctaatacatg tgctatgtag gtatgcgttt 3480
 cctgatctca aaacacgtct agaacgggaa agaaaagcac aggcataaat ggataagtta 3540
 cttgctaaac aaaacgagtc attagttaat aataaacaag aagaaaagag tgaaaaagag 3600
 cctgacatat tgtcagaagg tgatactcag ccattaggat gccattgttc aaattcagat 3660
 aaattgaatg atgagctctg agagttgcta gaggaacaac aggatcaact acagagttaa 3720
 cagctaccac aacttggtgc tagccctact gtatgtgaac aagatgagat aagtcaagtt 3780
 gagtctacaa tggaaggggt acatccctact gggtcaccgt gttgtcgaag acggggtcta 3840
 acttctctag ttagtgatgt tatcattgag caacagggtta atagccaagg taaggagtag 3900
 ttttaacagg tgggttattt tagtaaagga gaatcagttg ttgacagttg gagatctatc 3960
 tgttgtcaaa gatagaaaat gtgttagaaa agaattactt atagaagtta tataattttt 4020
 ttttagtatct aattaagtag gattgtagat atatggtgtt gttattatac aatattgtta 4080
 agtctcatga aatgatgct atcaaattgt taatgctatc ataagggtta ttaaatgaaa 4140
 aatctgtata acgtttttata ttcttttttag ttatgaattt atgtaataa tgtatttgaa 4200
 tactctaaat tccatttagt taagacaaat tgacttatga gaatgataag tatttagtta 4260

atgatttttgc tgtgatatgt attaagtgag tagcgttaga cttgtctttt tcattatttt 4320
 tgtatataat gtagtgtatt agttaaataa tgggtctgtat tatgcattct gattattaca 4380
 ctttagctat tataggttca gtaggttttag cactaatcat actttttgtta tgtgttagtc 4440
 aacttatcaa atatgcgatac 4460

<210> 75
 <211> 726
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(726)
 <223> Corresponds to SEQ ID NO:74, nucleotides 369..1094
 Hypothetical outer membrane protein
 Product = "27hworf1"

<400> 75
 atg aaa ctt tct ttg tat ata gtt agt act ata ggt gtg att ata ttg 48
 Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu
 1 5 10 15
 tta ctt tgc ttg atg tta att ttg tat tgt atc gat att gca tat gct 96
 Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala
 20 25 30
 aat att aaa aac tgt gtt ttc aat aat act gat aaa act aaa aat gct 144
 Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala
 35 40 45
 gtg aat tta tct att gaa aac agg gtt aaa aac tct gtt tta tgt ggt 192
 Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly
 50 55 60
 cta aaa aaa gaa ttt aga agt aca tta aga aat ttt tgt gat tat aac 240
 Leu Lys Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn
 65 70 75 80
 aat gtt aac tct gta gaa gca aaa tct gct caa tat ggt agt ctg atg 288
 Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met
 85 90 95
 gta aaa gct ggt tct aaa tac atc caa gat tta ata tct gaa ata gat 336
 Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp
 100 105 110
 gac cga att gtt aat cag tat att act ggg agg gta tta tca cta gaa 384
 Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu
 115 120 125

gta tta ata atg caa ttt gag gat aca ata tat act ata tgt aat gag 432
Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu
130 135 140

gaa act ata cag tgc gaa cta caa aga gtg cta tat gta cgt ttg ctt 480
Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu
145 150 155 160

tta aat aat att tta aag ttg aca aaa agt ata tgt gaa caa agt gat 528
Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp
165 170 175

att gaa tta atg gaa ata tat gga atg aaa ttt gaa tat gct tta tct 576
Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser
180 185 190

ttt att cat agt ggt ttt act tat ata atg aaa aat ata tgt aca tta 624
Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu
195 200 205

agt ggt aat gtt tat tgt aat aat caa aaa cag ttg tgt act gat gat 672
Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp
210 215 220

gtt act ttt act act ata tca tta tat gat ata aac cat tgt att agt 720
Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser
225 230 235 240

cat tag 726
His

<210> 76
<211> 241
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 76

Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu
1 5 10 15

Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala
20 25 30

Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala
35 40 45

Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly
50 55 60

Leu Lys Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn
65 70 75 80

Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met
85 90 95

Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp
100 105 110

Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu
115 120 125

Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu
130 135 140

Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu
145 150 155 160

Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp
165 170 175

Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser
180 185 190

Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu
195 200 205

Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp
210 215 220

Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser
225 230 235 240

His

<210> 77

<211> 567

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(567)
 <223> Complement to SEQ ID NO:74, nucleotides 2149..2715
 Hypothetical DNA-3-methyladenine glycosidase
 Product = "27hworf2"

<400> 77
 ttaagttagt gtaggtacta gtttggtgtc aatgtattgt agtgaagtaa cgtcaggaat 60
 tacaaatctc cagaatttat ctgttgcctt actaatgcct attctggggg tgcaaata 120
 atcatctata ttgagatttg tattacaaat gcagaaacta tgatttgctg tcatgtctat 180
 attgttatgt tcttttggtt tgtgtagggg ttacatatt tttcctgggc cattaacttt 240
 tgtatgtggt gtatttttag ataataagat tatacttcga attaatttg ctgcagggaa 300
 accttcaggt tctgtaacaa cgttgaggca gtgatacatt ccatagatta aataaacata 360
 agagaatcca gggttaccaa acattacagc agtgcgcttt gtatatccgt ggaaagaatg 420
 tgctgcttga tcatcttgct ctatatatgc ttctgtttct gttataatcc ctttgtgttg 480
 attaaaaagt aacatcttgc ctagtaagct gcttgcaaca tcaagtgatt tttgtttata 540
 aatgacttc tttaatatgt tgtacat 567

<210> 78
 <211> 240
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> misc_feature
 <222> (1)..(240)
 <223> Complement to SEQ ID NO:74, nucleotides 3369..3608
 Product = "27hworf4"

<400> 78
 ttaatggtgt gttatgccgt atagagattt tgctataact tggtagcta tattgatagc 60
 gtgtatcatc acgatatgtg tactaataca tgtgctatgt aggtatgcgt ttcctgatct 120
 caaaacacgt ctagaacggg aaagaaaagc acaggcaaaa atggataagt tacttgctaa 180
 acaaaacgag tcattagtta ataataaaca agaagaaaag agtgaaaaag agcctgacat 240

<210> 79
 <211> 519
 <212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(519)

<223> Corresponds to SEQ ID NO:74, nucleotides 3382..3900
Hypothetical lipoprotein
Product = "27hworf3"

<400> 79

atg ccg tat aga gat ttt gct ata act tgg tta gct ata ttg ata gcg	48
Met Pro Tyr Arg Asp Phe Ala Ile Thr Trp Leu Ala Ile Leu Ile Ala	
1 5 10 15	

tgt atc atc acg ata tgt gta cta ata cat gtg cta tgt agg tat gcg	96
Cys Ile Ile Thr Ile Cys Val Leu Ile His Val Leu Cys Arg Tyr Ala	
20 25 30	

ttt cct gat ctc aaa aca cgt cta gaa cgg gaa aga aaa gca cag gca	144
Phe Pro Asp Leu Lys Thr Arg Leu Glu Arg Glu Arg Lys Ala Gln Ala	
35 40 45	

aaa atg gat aag tta ctt gct aaa caa aac gag tca tta gtt aat aat	192
Lys Met Asp Lys Leu Leu Ala Lys Gln Asn Glu Ser Leu Val Asn Asn	
50 55 60	

aaa caa gaa gaa aag agt gaa aaa gag cct gac ata ttg tca gaa ggt	240
Lys Gln Glu Glu Lys Ser Glu Lys Glu Pro Asp Ile Leu Ser Glu Gly	
65 70 75 80	

gat act cag cca tta gga tgc cat tgt tca aat tca gat aaa ttg aat	288
Asp Thr Gln Pro Leu Gly Cys His Cys Ser Asn Ser Asp Lys Leu Asn	
85 90 95	

gat gag tct gta gag ttg cta gag gaa caa cag gat caa cta cag agt	336
Asp Glu Ser Val Glu Leu Leu Glu Gln Gln Asp Gln Leu Gln Ser	
100 105 110	

gaa cag cta cca caa ctt gtg tct agc cct act gta gtt gaa caa gat	384
Glu Gln Leu Pro Gln Leu Val Ser Ser Pro Thr Val Val Glu Gln Asp	
115 120 125	

gag ata agt caa gtt gag tct aca atg gaa ggg tta cat cct act ggt	432
Glu Ile Ser Gln Val Glu Ser Thr Met Glu Gly Leu His Pro Thr Gly	
130 135 140	

tca ccg tgt tgt cga aga cgg gct cta act tct cta gtt agt gat gtt	480
Ser Pro Cys Cys Arg Arg Arg Ala Leu Thr Ser Leu Val Ser Asp Val	
145 150 155 160	

atc att gag caa cag ggt aat agc caa ggt aag gag tag	519
Ile Ile Glu Gln Gln Gly Asn Ser Gln Gly Lys Glu	
165 170	

<210> 80
 <211> 172
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 80

Met Pro Tyr Arg Asp Phe Ala Ile Thr Trp Leu Ala Ile Leu Ile Ala
 1 5 10 15

Cys Ile Ile Thr Ile Cys Val Leu Ile His Val Leu Cys Arg Tyr Ala
 20 25 30

Phe Pro Asp Leu Lys Thr Arg Leu Glu Arg Glu Arg Lys Ala Gln Ala
 35 40 45

Lys Met Asp Lys Leu Leu Ala Lys Gln Asn Glu Ser Leu Val Asn Asn
 50 55 60

Lys Gln Glu Glu Lys Ser Glu Lys Glu Pro Asp Ile Leu Ser Glu Gly
 65 70 75 80

Asp Thr Gln Pro Leu Gly Cys His Cys Ser Asn Ser Asp Lys Leu Asn
 85 90 95

Asp Glu Ser Val Glu Leu Leu Glu Glu Gln Gln Asp Gln Leu Gln Ser
 100 105 110

Glu Gln Leu Pro Gln Leu Val Ser Ser Pro Thr Val Val Glu Gln Asp
 115 120 125

Glu Ile Ser Gln Val Glu Ser Thr Met Glu Gly Leu His Pro Thr Gly
 130 135 140

Ser Pro Cys Cys Arg Arg Arg Ala Leu Thr Ser Leu Val Ser Asp Val
 145 150 155 160

Ile Ile Glu Gln Gln Gly Asn Ser Gln Gly Lys Glu
 165 170

<210> 81
 <211> 560
 <212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc_feature

<222> (560)..(560)

<223> n = a, c, g, or t

<400> 81

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gatccataat ctcacataata acccctgttaa ttgaggtatt agtagaaata ttagctatat      60
cacaccaagc attttcaata atttctttaa aatcagaagt atttaccata ttcacataacc      120
tcaacttaac aacacagatt tattattata aacactatta aaaaaataac aagatacaca      180
ctatgaatca gataaccttg gtattctaata atacgtatga tataatgata ctaaaccata      240
agtttatatt atttaaagac ataatgacat atctttaaat gctaatatgt ataattcttaa      300
agtccttaag atacatacat ttatagacat atctgtaata atgcactata taatgttaag      360
atgtatagtc aataagtttg tgtttaatga gaatagaatg caaaaattgc aaagcagttt      420
atagaataga caatagcaaa attccatta atggtaaaaa agttaagtt aaatgcacaa      480
actgtaatac tacatggatg cacataccaa ctcaagataa agcaatacct gaagaagaaa      540
aacaattagt aataggatcn      560

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<210> 82

<211> 174

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(174)

<223> Corresponds to SEQ ID NO:81, nucleotides 387..>559
Product = "lgdorfli"

<220>

<221> misc_feature

<222> (174)..(174)

<223> n = a, c, g, or t.

<220>

<221> misc_feature

<222> (172)..(174)

<223> Xaa = Ser

<400> 82


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<210>      83
<211>      58
<212>      PRT
<213>      Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221>      misc_feature
<222>      (58)..(58)
<223>      The 'Xaa' at location 58 stands for Ser.

<220>
<221>      misc_feature
<222>      (174)..(174)
<223>      n = a, c, g, or t.

<220>
<221>      misc_feature
<222>      (172)..(174)
<223>      Xaa = Ser

<400>      83

Met Arg Ile Glu Cys Lys Asn Cys Lys Ala Val Tyr Arg Ile Asp Asn
1              5              10              15

Ser Lys Ile Pro Ile Asn Gly Lys Lys Val Lys Val Lys Cys Thr Asn
      20              25              30

Cys Asn Thr Thr Trp Met His Ile Pro Thr Gln Asp Lys Ala Ile Pro
      35              40              45

Glu Glu Glu Lys Gln Leu Val Ile Gly Xaa
      50              55

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<210> 84
 <211> 2008
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 84
 gatcaaaaag ggataccaaa agagcaatac tatataaaat tagtatctgt taattcaaca 60
 tatectgact caattaataa cttactcata tttagtagta ttattgaaag ctatgaaggc 120
 actgtgaaca aatttcgttg tggagatact gtaagtataa agtacgatat acgtgaacta 180
 aacggtaata cgatactaca agatcaagaa ttaaaattta ctattggaaa aaatgaagtc 240
 cctcttgcaa tagagctagg tgtaattaat atgagacaag acatggcaag acatattatt 300
 gcaccattag aacttttgac taattttgac aaacctgaca acttttgatg aatacaaaat 360
 aaaactaatt gatattacct acattaatca accacaacct atacaaaaaa acgcaaagcc 420
 cageccaatct taagggtgatt atttcttata tctgtatagc cacataaaaa agctaaaaat 480
 aacggttatta tatcaaataa attacaatca acaatactac actaatatta tagaaatcta 540
 ctaatatatt gatatagtaa aataatacac atttacacaa tcaatactta aattcataat 600
 aacttggtgc aactttataa aaccagctat ttcataaaaa taacacaaaa ctataaaaca 660
 ccaaatagct tactcacgct aaatgtttct ataaataaat caacttgta ttgtaataat 720
 ataaaaactc accaatttta ataaaacaaa tatatactaa tcttttattt cctaatttat 780
 cttaataaga ttcaatatcc ttatacta ataaatctta actcatatat taccacccca 840
 cactaacaaa tccatagaac ttgctaagtg tatattatat aatattaatt taacatgta 900
 atgactgaaa aagtattaac ttaaagatct atttaataaa atttaacctc ttctataacc 960
 ttaactatca tcatttttaa gtaactgaag tatttaagac atttaacaat tatatatcat 1020
 ataaaaatct ttaatgtact agcaattgat gaattatgcc ctcataatat atgcaagcat 1080
 aaaatgccta ttttaacaaa actttatcta ttctataacc ttaactatta ccatttttaa 1140
 gtaactgagg tatttaagac atttaataat tatataccat ataaaaatct gcttaatgta 1200
 ctagcaattg atgaattatt ccttcataat atatgcaagc ataaaatgcc taatttaaca 1260
 aaactttatc tattctataa ccttaactat tactattttc aagtaactga agtatttaag 1320
 atatttgaca attatatatc atattaaaat ctgcttaatg tactagcaat tgatggatta 1380
 ttctctcata atatatgtaa gcataaaatg cctaatttaa taaaacttta tctattctat 1440
 aacttaacta ttactatttt caagtaactg aagtatttaa gatatttgac aattatatat 1500

catatcaaaa tctgcttaat gtactagcaa ttgatggatt attctctcat aatatatgta 1560
 agcataaaat gcctaattta ataaaacttt atctattcta taaccttaac tattactatt 1620
 ttcaagtaac tgaagtattt aagatatttg acaattatat atcatataaa aatctttaat 1680
 gtactagcaa ttgacaacta tgccttgata atctatgtag cataaaatac ctcatttaac 1740
 aaaactttat ctattctata accttaacta ttaccatttt taagtaactg aagtatttaa 1800
 gatatttgac aattatatat catataaaaa tctttaatgt actagcaatt gacaactatt 1860
 ccctgataat ctatgtagca taaaatacct acaggaatct ttattaatag taatttactt 1920
 atctattgaa cataacttta agtattacta gtcataatat tataaagaca catttaatat 1980
 taaacattgt agacatttta acatgatc 2008

<210> 85
 <211> 348
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(348)
 <223> Corresponds to SEQ ID NO:84, nucleotides <1..348
 Product = "2gdorfli"

<400> 85
 gat caa aaa ggg ata cca aaa gag caa tac tat ata aaa tta gta tct 48
 Asp Gln Lys Gly Ile Pro Lys Glu Gln Tyr Tyr Ile Lys Leu Val Ser
 1 5 10 15
 gtt aat tca aca tat cct gac tca att aat aac tta ctc ata ttt agt 96
 Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser
 20 25 30
 agt att att gaa agc tat gaa ggc act gtg aac aaa ttt cgt tgt gga 144
 Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly
 35 40 45
 gat act gta agt ata aag tac gat ata cgt gaa cta aac ggt aat acg 192
 Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr
 50 55 60
 ata cta caa gat caa gaa tta aaa ttt act att gga aaa aat gaa gtc 240
 Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val
 65 70 75 80
 cct ctt gca ata gag cta ggt gta att aat atg aga caa gac atg gca 288
 Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala

85

90

95

aga cat att att gca cca tta gaa ctt ttg act aat ttt gac aaa cct 336
 Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro
 100 105 110

gac aac ttt tga 348
 Asp Asn Phe
 115

<210> 86

<211> 115

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 86

Asp Gln Lys Gly Ile Pro Lys Glu Gln Tyr Tyr Ile Lys Leu Val Ser
 1 5 10 15

Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser
 20 25 30

Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly
 35 40 45

Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr
 50 55 60

Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val
 65 70 75 80

Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala
 85 90 95

Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro
 100 105 110

Asp Asn Phe
 115

<210> 87

<211> 3829

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 87
gatctacaaa tgaaaagtgt atgggttaact ttacaataat ggattggtga aagtaaattt 60
gacaaattaa tcaatacctt aaaatgagtt gagtggaaaa gtataaataa tgtaggtggt 120
ttttttgttt ataattgaat taaagtgctt aaagatattt atatagttat tacttagatt 180
atttaattaa attaagctag tgaacaaaga atttgtatta tatatatattt aggtatctat 240
tatctttaca gtttaaataa gaaagcaagg gtttattaat tatatagtga atgaaatata 300
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gttgcttata	ggttctgggt	tatctatagt	gtatgtttgg	aaaatagttg	aagcagtgtg		1920
tcttcgttca	cctgataata	aggtagttat	gtcgtcgttt	gaaacaccaa	atgttatggg		1980
attatgtatt	tggataatgg	taattgcttc	gattattgtg	ggaatatatc	caattccttt		2040
aacattgatt	tctaataaaa	tagcgacgtt	gctattatat	tgagatatct	atttgaattt		2100
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caattaacta	cccattccta	ggtaattttat	acctaactat	taactaatca	ttcttatgag		2220
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taataataag	ttataaaaaat	catttagcat	aacattatct	taaataacca	taacacaact		2640
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caaatttgta	tttaacaatt	gatattgact	acttaataag	tgaatctatt	attttagcaa		3240
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cttcttgatc tgatccaagt tcgatatcaa tgtgcttttt tcctaacata ttgctgttta 3360
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 aataccgatg ttaatatggt ttgtgttatt taaaagactt ttgaggatgg taggcgtact 3720
 tagttccggt taaatttggt acatgtagat ttttttctgc aagtgttggg aattgattat 3780
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<210> 88
 <211> 1479
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(1479)
 <223> Corresponds to SEQ ID NO:87, nucleotides 605..2083
 Hypothetical NADH dehydrogenase (ubiquinone)
 Product = "3gdorf1"

<400> 88
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 Met Ser Ser Ser Leu Pro Val Leu Gln Val Ile Ile Pro Leu Leu Ser
 1 5 10 15
 gca gta ata tgt gct tta tta aaa aat agt aca ttg gtg aaa att ata 96
 Ala Val Ile Cys Ala Leu Leu Lys Asn Ser Thr Leu Val Lys Ile Ile
 20 25 30
 tca tct att gtt gta gta gta tct ttt tcc att gcg ttg gta ttg ttc 144
 Ser Ser Ile Val Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe
 35 40 45
 tct cag gtt tat tct gct gat gta atc aaa tac agc cta ggg ggg tgg 192
 Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp
 50 55 60
 gtc gtt cct tat ggc ata gaa ctt aaa gtg aac ata ttt agt gct act 240
 Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr
 65 70 75 80
 atg ctt gtt tta gta aat ttt att gct gta atg agt ata ttg tat ggc 288

Met Leu Val Leu Val Asn Phe Ile Ala Val Met Ser Ile Leu Tyr Gly
85 90 95

ata tat cct aac atc aga gaa ata ggt gtt aac aag ata cca agt ttc 336
Ile Tyr Pro Asn Ile Arg Glu Ile Gly Val Asn Lys Ile Pro Ser Phe
100 105 110

tat tct gta ttt ttg cta tgt tta ggt ggc ttt ttg ggg ata tta gta 384
Tyr Ser Val Phe Leu Leu Cys Leu Gly Gly Phe Leu Gly Ile Leu Val
115 120 125

tca aat gat gtt ttt aat atc tat gtt ttt ctt gag att tcg tct att 432
Ser Asn Asp Val Phe Asn Ile Tyr Val Phe Leu Glu Ile Ser Ser Ile
130 135 140

tct tct tat att ttg gtt gca atg gga aaa gat aaa gct gct tta ata 480
Ser Ser Tyr Ile Leu Val Ala Met Gly Lys Asp Lys Ala Ala Leu Ile
145 150 155 160

gca gca ttt gat tat tta gta att ggt aca att ggg gca act ttt tat 528
Ala Ala Phe Asp Tyr Leu Val Ile Gly Thr Ile Gly Ala Thr Phe Tyr
165 170 175

tta ata ggt ata ggc ttt ttg tat gct att act ggt aca ttg aat att 576
Leu Ile Gly Ile Gly Phe Leu Tyr Ala Ile Thr Gly Thr Leu Asn Ile
180 185 190

gga gat ttg ttt cta ata att cat gat aat ttg ctg gta aca aat aga 624
Gly Asp Leu Phe Leu Ile Ile His Asp Asn Leu Leu Val Thr Asn Arg
195 200 205

gtt aca cag att gca atg tta ttt att atg gta ggt ttg ttt ata aag 672
Val Thr Gln Ile Ala Met Leu Phe Ile Met Val Gly Leu Phe Ile Lys
210 215 220

aca gcg cta ttc cca ttt cat aaa tgg tta ata cag gct tat agt ttt 720
Thr Ala Leu Phe Pro Phe His Lys Trp Leu Ile Gln Ala Tyr Ser Phe
225 230 235 240

gct cct tct ttt att tct gtg ttt ttt tcc ggt act tct act aaa gtt 768
Ala Pro Ser Phe Ile Ser Val Phe Phe Ser Gly Thr Ser Thr Lys Val
245 250 255

atg ata tat cta att ata aag atg ata tat gac gtt ttt aaa gct gat 816
Met Ile Tyr Leu Ile Ile Lys Met Ile Tyr Asp Val Phe Lys Ala Asp
260 265 270

ttt gtt ttt gtg act tta cct ttt aat att gtt ttt atg tgt ttt gct 864
Phe Val Phe Val Thr Leu Pro Phe Asn Ile Val Phe Met Cys Phe Ala
275 280 285

gtg ttg tca ata gtt tgt gga tct tta ctt gca att ttt act agc aat 912
Val Leu Ser Ile Val Cys Gly Ser Leu Leu Ala Ile Phe Thr Ser Asn
290 295 300

att aaa aag ata ttt gct tat tca agt att gca cat tta gga tat att 960
 Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile
 305 310 315 320

gta ttt gca gtt agt tta aat act aat tat ggt ttg gtt gca gct ata 1008
 Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile
 325 330 335

gct tat att att agt cat agc ttg gtt aag tca gca tta ttt atg att 1056
 Ala Tyr Ile Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile
 340 345 350

gta ggt agc att gat tat agt tgt ggt aac aga cat ctg aaa gat tgt 1104
 Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys
 355 360 365

gca aac atg tgg gaa acc atg cca aaa att aca ttg cca ttt att ata 1152
 Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile
 370 375 380

tta tgt tta agt tta att ggt atg cca gtt act tca ggg ttt att gct 1200
 Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala
 385 390 395 400

aaa tgg tat att gtt gat gca gtt ata aag tct aat ttt tgg gtt ggt 1248
 Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly
 405 410 415

att ttt gtg ttg ctt ata ggt tct ggg tta tct ata gtg tat gtt tgg 1296
 Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp
 420 425 430

aaa ata gtt gaa gca gtg tgt ctt cgt tca cct gat aat aag gta gtt 1344
 Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val
 435 440 445

atg tcg tcg ttt gaa aca cca aat gtt atg gta tta tgt att tgg ata 1392
 Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile
 450 455 460

atg gta att gct tcg att att gtg gga ata tat cca att cct tta aca 1440
 Met Val Ile Ala Ser Ile Ile Val Gly Ile Tyr Pro Ile Pro Leu Thr
 465 470 475 480

ttg att tct aat aaa ata gcg acg ttg cta tta tat tga 1479
 Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr
 485 490

<210> 89

<211> 492

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 89

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Ala Val Ile Cys Ala Leu Leu Lys Asn Ser Thr Leu Val Lys Ile Ile
20 25 30

Ser Ser Ile Val Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe
35 40 45

Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp
50 55 60

Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr
65 70 75 80

Met Leu Val Leu Val Asn Phe Ile Ala Val Met Ser Ile Leu Tyr Gly
85 90 95

Ile Tyr Pro Asn Ile Arg Glu Ile Gly Val Asn Lys Ile Pro Ser Phe
100 105 110

Tyr Ser Val Phe Leu Leu Cys Leu Gly Gly Phe Leu Gly Ile Leu Val
115 120 125

Ser Asn Asp Val Phe Asn Ile Tyr Val Phe Leu Glu Ile Ser Ser Ile
130 135 140

Ser Ser Tyr Ile Leu Val Ala Met Gly Lys Asp Lys Ala Ala Leu Ile
145 150 155 160

Ala Ala Phe Asp Tyr Leu Val Ile Gly Thr Ile Gly Ala Thr Phe Tyr
165 170 175

Leu Ile Gly Ile Gly Phe Leu Tyr Ala Ile Thr Gly Thr Leu Asn Ile
180 185 190

Gly Asp Leu Phe Leu Ile Ile His Asp Asn Leu Leu Val Thr Asn Arg
195 200 205

Val Thr Gln Ile Ala Met Leu Phe Ile Met Val Gly Leu Phe Ile Lys
210 215 220

Thr Ala Leu Phe Pro Phe His Lys Trp Leu Ile Gln Ala Tyr Ser Phe
225 230 235 240

Ala Pro Ser Phe Ile Ser Val Phe Phe Ser Gly Thr Ser Thr Lys Val
245 250 255

Met Ile Tyr Leu Ile Ile Lys Met Ile Tyr Asp Val Phe Lys Ala Asp
260 265 270

Phe Val Phe Val Thr Leu Pro Phe Asn Ile Val Phe Met Cys Phe Ala
275 280 285

Val Leu Ser Ile Val Cys Gly Ser Leu Leu Ala Ile Phe Thr Ser Asn
290 295 300

Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile
305 310 315 320

Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile
325 330 335

Ala Tyr Ile Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile
340 345 350

Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys
355 360 365

Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile
370 375 380

Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala
385 390 395 400

Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly
405 410 415

Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp
420 425 430

Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val

435

440

445

Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile
 450 455 460

Met Val Ile Ala Ser Ile Ile Val Gly Ile Tyr Pro Ile Pro Leu Thr
 465 470 475 480

Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr
 485 490

<210> 90
 <211> 300
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(300)
 <223> Complement to SEQ ID NO:87, nucleotides 2311..2610
 Product = "3gdorf2"

<400> 90
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 agttgtactg tgtgcaacat gatgttctgg agtataattc ctatcaaag gtttatccat 120
 actacctata ttttcttgag tacttacaga tgattgatct ttaggttgaa gctttttctt 180
 aagtttttta ttgtacttaa agaaataagt actacctatc actaatagaa gtattagtaa 240
 cgctattgac tttgggttac taactatata taataataag ttataaaaat catttagcat 300

<210> 91
 <211> 450
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> misc_feature
 <222> (1)..(450)
 <223> Complement to SEQ ID NO:87, nucleotides 3209..3658
 Hypothetical outer membrane protein, related to proposed ABC tran
 sporter
 Product = "3gdorf3"

<400> 91
 ctacttaata agtgaatcta ttatttttagc aataattgca ttgaaactta aatctgaatg 60

tgtatgttct attaaacctt cacttacgat gacttcttga tctgatccaa gttcgatata 120
aatgtgcttt tttcctaaca tattgctggt taatatagat gctgaactat ctgaaggtag 180
taagatattt ttctgtatgc acattgttac tataggagta tagctttcat tcaatgatat 240
tgaagttact gtacctattt ttactcctga tattgttact tcctctccta tgtccaaccc 300
atctacattt gagaaaaatg ctttaactgt ataacaatta cgcaagggtat ttttatatgg 360
taatttggtta aatgctatta tcccaataga tattgctcct gctaacta ggaatcctat 420
aaaaatttca ataattttg atctatgcat 450

<210> 92
<211> 226
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 92
gatcaagctt taaatcattt ccaatcattg ataccttagt aagaacatca ggaccattac 60
ctataatagt agcaccttta ataggagatg taactttccc atcttctatt aagtagcttt 120
cagaagctga aaaaacaaat ttaccagatg taatatctac ctgaccacca gcaaaattca 180
cagcataaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 93
<211> 226
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(226)
<223> Complement to SEQ ID NO:92, nucleotides <1..>226
Hypothetical tldD protein
Product = "4gdorf1i"

<400> 93
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ctataatagt agcaccttta ataggagatg taactttccc atcttctatt aagtagcttt 120
cagaagctga aaaaacaaat ttaccagatg taatatctac ctgaccacca gcaaaattca 180
cagcataaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 94

<211> 160
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 94
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 gagcagcccg gcgtggccga gctggggcgac gccgtcgggc gtcgacagcg tgcccatatg 120
 cgccgtgatc ggcaggccgt gggcgcgggc gaactcgatc 160

<210> 95
 <211> 299
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 95
 gatctatgga aaacatcctt gtgttgctgc actacaaaat ataaatagaa aatgtcatga 60
 gcttttagtt acagaaaatt tcattaaaca taacaatgga atacaaaaaa ttagagagct 120
 tagtaaacia aaaaatattt acccaaaaaca agtaaataac aatactatca actcagtact 180
 accacctaag agtaaccacc aaggcattgc tttaacaagtt tcaatagtag atacagtaag 240
 catagaagac gtattatcta atattcctac agagatttca acaataatac ttttagatc 299

<210> 96
 <211> 297
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
 <221> CDS
 <222> (1)..(297)
 <223> Corresponds to SEQ ID NO:95, nucleotides <1..>297
 Product = "6gdorfli"

<400> 96
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 Ile Tyr Gly Lys His Pro Cys Val Ala Ala Leu Gln Asn Ile Asn Arg
 1 5 10 15
 aaa tgt cat gag ctt tta gtt aca gaa aat ttc att aaa cat aac aat 96
 Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn
 20 25 30
 gga ata caa aaa att aga gag ctt agt aaa caa aaa aat att tac cca 144
 Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro
 35 40 45
 aaa caa gta aat atc aat act atc aac tca gta cta cca cct aat agt 192

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser
 50 55 60

aac cac caa ggc att gct tta caa gtt tca ata gta gat aca gta agc 240
 Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser
 65 70 75 80

ata gaa gac gta tta tct aat att cct aca gag att tca aca ata ata 288
 Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile
 85 90 95

ctt tta gat 297
 Leu Leu Asp

<210> 97
 <211> 99
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 97

Ile Tyr Gly Lys His Pro Cys Val Ala Ala Leu Gln Asn Ile Asn Arg
 1 5 10 15

Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn
 20 25 30

Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro
 35 40 45

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser
 50 55 60

Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser
 65 70 75 80

Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile
 85 90 95

Leu Leu Asp

<210> 98
 <211> 2104
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 98
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cattttacca gaatgatgaa taatgacatt tcataaagtt taataaataa ggatttataa 180
tgaatgctaa agaaaaaat attagagaag aaatttttaa tcttcaaaaa aagattgctg 240
aatgagacaa tgcttattat aatttggata atcctattgt aactgatgaa atttatgata 300
ctgagtttat tagacttcaa aaattagaaa aacaatatag tcatttgcta acttatgaag 360
aagttaaaaa ctctccaacg caaaaaattg atgcaaagtc tttatcaata tttgataaag 420
taattcataa aaaaccaatg ctttctttaa acaaagcata ttcaattgaa gaaattaaga 480
aattttattaa aaagattgaa aaatatacta atgatttttc attttttatt gaacctaaaa 540
ttgatggtct ttctatttca ttaacttatg aaaatggaaa actaattaga ggtgtaacta 600
gaggagatgg aataacagga gaagatgtta caaaaaatat ttacaaatt aatgatatcc 660
ctaaagaaat agaatacaaa cacaaaatcg aattaagagg aaaaatatat ttatctattt 720
ctagatttaa tgaattaaat gaagaaaatt taaaaataa tttaccgcct ttagctaacc 780
caagaaatgc agcagccgga actttaagac aattagattc taatattggt tctcaaagag 840
ggttgtcatc ttttatatat tttgtagtcg atgctcccag tcataatatt tggacaatgg 900
aagatgcctt ttgttttctt aagaaaaata attttcatgt tgtaaaagat tataaactag 960
ctaaaaatat taatcaaatt gaagaatata taaataattt tccagaactt aaaaaaacat 1020
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gatc 2104

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<211> 642
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<223> Corresponds to SEQ ID NO:98, nucleotides 180..>2104
Hypothetical DNA ligase
Product = "7gdorfli"

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Ile Val Thr Asp Glu Ile Tyr Asp Thr Glu Phe Ile Arg Leu Gln Lys
35 40 45

Leu Glu Lys Gln Tyr Ser His Leu Leu Thr Tyr Glu Glu Val Lys Asn
50 55 60

Ser Pro Thr Gln Lys Ile Asp Ala Lys Ser Leu Ser Ile Phe Asp Lys
65 70 75 80

Val Ile His Lys Lys Pro Met Leu Ser Leu Asn Lys Ala Tyr Ser Ile
 85 90 95

Glu Glu Ile Lys Lys Phe Ile Lys Lys Ile Glu Lys Tyr Thr Asn Asp
 100 105 110

Phe Ser Phe Phe Ile Glu Pro Lys Ile Asp Gly Leu Ser Ile Ser Leu
 115 120 125

Thr Tyr Glu Asn Gly Lys Leu Ile Arg Gly Val Thr Arg Gly Asp Gly
 130 135 140

Ile Thr Gly Glu Asp Val Thr Lys Asn Ile Leu Gln Ile Asn Asp Ile
 145 150 155 160

Pro Lys Glu Ile Glu Tyr Lys His Lys Ile Glu Leu Arg Gly Lys Ile
 165 170 175

Tyr Leu Ser Ile Ser Arg Phe Asn Glu Leu Asn Glu Glu Asn Leu Lys
 180 185 190

Asn Asn Leu Pro Pro Leu Ala Asn Pro Arg Asn Ala Ala Ala Gly Thr
 195 200 205

Leu Arg Gln Leu Asp Ser Asn Ile Val Ser Gln Arg Gly Leu Ser Ser
 210 215 220

Phe Ile Tyr Phe Val Val Asp Ala Pro Ser His Asn Ile Trp Thr Met
 225 230 235 240

Glu Asp Ala Phe Cys Phe Leu Lys Lys Asn Asn Phe His Val Val Lys
 245 250 255

Asp Tyr Lys Leu Ala Lys Asn Ile Asn Gln Ile Glu Glu Tyr Ile Asn
 260 265 270

Asn Phe Pro Glu Leu Lys Lys Thr Phe Asp Phe Glu Ala Asp Gly Val
 275 280 285

Val Ile Lys Leu Asn Glu Ile Lys Trp Trp Asn Lys Ile Gly Gln Thr
 290 295 300

Gln Lys Phe Pro His Tyr Ala Ile Ala Phe Lys Phe Glu Pro Asn Ile
305 310 315 320

Glu Ile Thr Thr Ile Lys Lys Ile Phe Ile Thr Ile Gly Arg Thr Gly
325 330 335

Leu Val Thr Tyr Asn Gly Gln Val Lys Thr Val Glu Ile Ser Gly Ser
340 345 350

Lys Ile Asn Phe Ala Thr Leu Asn Asn Phe Asn Tyr Val Lys Glu Leu
355 360 365

Asn Leu Asn Val Gly Asp Glu Val Tyr Ile Lys Lys Ala Gly Glu Ile
370 375 380

Ile Pro Cys Ile Ile Gly Leu Val Asn Pro Lys Gly Lys Pro Asp Tyr
385 390 395 400

Phe Lys Arg Ile Glu Thr Cys Pro Tyr Cys Asn Ser Lys Leu Ile Glu
405 410 415

Ser Glu Thr Phe Leu Glu Glu Tyr Cys Glu Asn Tyr Asn Cys Pro Glu
420 425 430

Ile Ile Lys Lys Gln Leu Ile His Phe Ser Ser Lys Glu Cys Met Asn
435 440 445

Phe Phe Ser Met Gly Glu Lys Ile Val Glu Lys Leu Tyr Glu Asn Lys
450 455 460

Leu Ile Leu Ser Pro Leu Asp Phe Tyr Asn Leu Lys Asn Asn Lys Asn
465 470 475 480

Glu Leu Thr Gln Leu Glu Lys Leu Gly Thr Lys Ser Ile Met Lys Ile
485 490 495

Leu Asp Ser Ile Glu Asp Ser Lys Lys Leu Gly Leu Asp Lys Phe Ile
500 505 510

Phe Ala Leu Ser Ile Lys His Ile Gly Gln Lys Val Ala Ser Phe Ile
515 520 525

Thr Ser Lys Val Gln Lys Leu Ser Glu Phe Leu Thr Phe Asp Phe Asp
530 535 540

Ser Leu Ile Gln Tyr Asn Glu Ile Gly Pro Lys Ile Ile Asp Ser Val
545 550 555 560

Lys Lys Trp Leu Ser Ala Glu Asn Asn Lys Lys Leu Ile Asn Asp Phe
565 570 575

Leu Asn Arg Gly Met Asn Phe Glu His Ile Ser Asn Ile Lys Ser Lys
580 585 590

Leu Leu Asp Gly Ile Asn Ile Val Ile Thr Gly Thr Leu Ser Lys Pro
595 600 605

Arg Asn Tyr Phe Glu Glu Leu Ile Lys Ala Asn Asn Gly Asn Ile Val
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625 630 635 640

Gly Ser

<210> 100

<211> 4055

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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ggacctgttc taatagctca tcttttatct ctacaacctt aataaaccat tggttactta 240

acaatatttc aataggcatt cctgatcgt cagcacattt cacatttgtt aatatttcct 300

ctttttttat cagtaaatta catttactta aggtttcaag taccagcttt cttgcttcta 360

ctattgatac tccatgtaat ttaccagata aagtatctgt ctctgcaatg ttatgtttta 420

gatcaagagt acctgattta cttattataa tctgcgtatt taaattatgt ttattccacc 480

aatatacatc taattcatca ccaaattgtac aacacattac aagaccagta cccttatcta 540
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 <211> 603
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <223> Corresponds to SEQ ID NO:100, nucleotides <1..605
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 ctt ttc gaa tac cat acc gga aac ggg att cca aaa tac ctt tgt cgc 96
 Leu Phe Glu Tyr His Thr Gly Asn Gly Ile Pro Lys Tyr Leu Cys Arg
 20 25 30
 gat atg cac cag tcc cag ttt aac cca tct atc cac att tct att tgc 144
 Asp Met His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys
 35 40 45
 tta cgc ata gac tgt gga tac caa tta atc tta cgg acc tgt tct aat 192
 Leu Arg Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn
 50 55 60
 agc tca tct ttt atc tct aca acc tta ata aac cat tgg tta ctt aac 240
 Ser Ser Ser Phe Ile Ser Thr Thr Leu Ile Asn His Trp Leu Leu Asn
 65 70 75 80
 aat att tca ata ggc att cct gat cgc tca gca cat ttc aca ttg tgt 288
 Asn Ile Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys
 85 90 95
 aat att tcc tct ttt ttt atc agt aaa tta cat tta ctt aag gtt tca 336
 Asn Ile Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser
 100 105 110
 agt acc agc ttt ctt gct tct act att gat act cca tgt aat tta cca 384
 Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro

115 120 125

gat aaa gta tct gtc tct gca atg tta tgt tta aga tca aga gta cct 432
 Asp Lys Val Ser Val Ser Ala Met Leu Cys Leu Arg Ser Arg Val Pro
 130 135 140

gat tta ctt att ata atc tgc gta ttt aaa tta tgt tta ttc cac caa 480
 Asp Leu Leu Ile Ile Ile Cys Val Phe Lys Leu Cys Leu Phe His Gln
 145 150 155 160

tat aca tct aat tca tca cca aat gta caa cac att aca aga cca gta 528
 Tyr Thr Ser Asn Ser Ser Pro Asn Val Gln His Ile Thr Arg Pro Val
 165 170 175

ccc tta tct att ttt act tgt tca tct gat aaa atc ggt act tta ttc 576
 Pro Leu Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe
 180 185 190

cca aat ata ggt act ata gca tac tga 603
 Pro Asn Ile Gly Thr Ile Ala Tyr
 195 200

<210> 102
 <211> 200
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 102

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Asp Met His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys
 35 40 45

Leu Arg Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn
 50 55 60

Ser Ser Ser Phe Ile Ser Thr Thr Leu Ile Asn His Trp Leu Leu Asn
 65 70 75 80

Asn Ile Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys
 85 90 95

Asn Ile Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser

100

105

110

Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro
 115 120 125

Asp Lys Val Ser Val Ser Ala Met Leu Cys Leu Arg Ser Arg Val Pro
 130 135 140

Asp Leu Leu Ile Ile Ile Cys Val Phe Lys Leu Cys Leu Phe His Gln
 145 150 155 160

Tyr Thr Ser Asn Ser Ser Pro Asn Val Gln His Ile Thr Arg Pro Val
 165 170 175

Pro Leu Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe
 180 185 190

Pro Asn Ile Gly Thr Ile Ala Tyr
 195 200

<210> 103
 <211> 1321
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <222> (1)..(1321)
 <223> n = a, c, g, or t

<220>
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 <222> (1)..(1321)
 <223> Complement to SEQ ID NO:100, nucleotides <1..1321
 Hypothetical valine-tRNA ligase
 Product = "3hworfli"

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 aacccatcta tccacatttc tatttgctta cgcatagact gtggatacca attaattcta 180
 cggacctgtt ctaatagctc atctttttatc tctacaacct taataaacca ttggttactt 240

aacaatattt caataggcat tcctgatcgc tcagcacatt tcacattgtg taatatttcc 300
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caatatacat ctaattcatc accaaatgta caacacatta caagaccagt acccttatct 540
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tattccagat cccaatcata actaatacca agagattgaa acaatatttt aaattccatt 960
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tcaataataa actgtttatc ttgtaaatc ttccatttat ataattttat tttatcccaa 1260
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a 1321

<210> 104
<211> 549
<212> DNA
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>
<221> misc_feature
<222> (1)..(549)
<223> Complement to SEQ ID NO:100, nucleotides 3508..>4055
Hypothetical glutamate-cysteine ligase
Product = "3hworf3i"

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 atttaggtta gagaatttat ctttaacagt attataccta tataaataac acgaaggagt 180
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 attgcgattt tttttattta acttcaatat gtcacacca caatatgcta caataattcc 360
 cattccatat gttccattat ctgcttttac aaacacatac ggttggtctg taatactgta 420
 taattgaaat ttattacgta tttcttgaat cataacatca actttatcag caatgtgttc 480
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<210> 105

<211> 4122

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 105

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 aaaagcgcta tagttttgct ttcatttttg taaaaaaaat taaagttgca atttaaatac 300
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ggaaaaaata aaagatatc aacgacatat taatctacct atatttcttg attatcaatc	2160
cacaactaaa acggatagta gagtcttaga tgctatgatt ccatattttc aagagttttc	2220
taatcctcat tcacgtagtc attgttttgg atggaaagct gagtcggctg ttgaattagc	2280
acgagaaaga attgcatctt taataaatgc tgaaagtaaa gaagtaatat tcacttctgg	2340
tgctacagaa tcaataaatt tggcaattaa aggtgtagca aacttttata aaagtaaagg	2400
aatcacatt attacagtac gtacagagca taaatgtggt ttagattcat gtcgccattt	2460
agaaacagaa ggatttgacg ttacttactt agatgtacaa aaaaatggta ttttagatct	2520
taatttatta aaatcagcta taactgataa gactatatgtg gtatcgggta tgatggtaaa	2580

caatgaaatt ggtgtcattc aaccaataga ggaaatagga aaaatttgtc ataatcatgg 2640
 agtattcttt catactgatg cagctcaagc atttggtaaa ataccaatag atgtaaacia 2700
 aatgaatata gatttgctta gtatatcagg acataaaata tatgtccaa tgggaatagg 2760
 ggcattatat gtacgtaaac gtcaaccaag aatacgactt actcctataa taaatgggtg 2820
 tggacaagaa cgtgggtatga gatctggaac catacctact ccattagcag taggtttagg 2880
 ggaagcagca tatatagctc aggaagtaat ggaagatgaa gccattagga taaaagaatt 2940
 gcgtgatatt ttatatagtg aaataaaaaa acattttacc tatgtaatac tgaatgggtg 3000
 ttatgaacia cgtatagcag gaaatttaaa ttttaagttt ccatatgtag aaggagaatc 3060
 tattattatg gcgattaaca acttagcagt aagttcagga tctgcttgta catctgcttc 3120
 actagaacca tcttatgttt tacgtgcgtt aaatatagat aaggatttag aacactcatc 3180
 tattagattt ggaataggta ggtttactac aaaagcagaa attttatatg cagcggatct 3240
 tattgtaaat agcataaaga ggttgctgta gatgagtcct ttatgggaaa tggtaacaag 3300
 aggtataaat cttaatgaaa ttaagtggga tgtgcattaa tttttattgt atttgataat 3360
 tatgaggtat ttatatgagt tacagtgagt ctcttctaga acattataag aatcctaaaa 3420
 atgttggtac ttacctaata gaggattaca atgtaggtac tggcttagtg ggagctccta 3480
 gctgtggtga tgtaatgaag ttacagatta aagtagatga taatggaaaa attatagatg 3540
 caaaatttaa aacttttgga tgtgggtgctg caattgcagc tagttcacta gctactgagt 3600
 taattaaagg taaaacagta gatgaggcac atgagttgaa aaatacagta ttggcaaaag 3660
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 cagctataaa tgactatcat atgaaacaag caaacaaaaa aaatgctact aaagatccta 3780
 atgaataata cagcaataat atgcaatcag gtttatctat ggataaagaa gtgttgatac 3840
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 tcacagataa gtctcctatt atcataacgg aaaatgctat taaaaaaatt aaggaactca 3960
 ttgataagaa aaaagattct gtcattggga ttagaataat ggtagcgcaa aaaggatggt 4020
 ttggttttaa gtataatata gaatatgcat atgatatcaa aatgttagat gtacaaattc 4080
 aagtaaaata tcaaaatcaa aattttataa ttttgattga tc 4122

<210> 106

<211> 1569
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(1569)

<223> Corresponds to SEQ ID NO:105, nucleotides 459..2027
 Hypothetical iron-sulfur co-factor synthesis
 Product = "11hworfl"

<400> 106

atg	ttg	atc	aca	gct	agg	cta	cgt	tat	gct	ata	atg	ttt	atg	gta	aaa	48
Met	Leu	Ile	Thr	Ala	Arg	Leu	Arg	Tyr	Ala	Ile	Met	Phe	Met	Val	Lys	
1				5					10					15		

ttg	gct	cat	ggg	ctt	tgc	acg	caa	caa	aat	aag	ttg	caa	cca	gta	aga	96
Leu	Ala	His	Gly	Leu	Cys	Thr	Gln	Gln	Asn	Lys	Leu	Gln	Pro	Val	Arg	
			20					25					30			

atg	tca	tat	att	gca	agt	aat	caa	tct	tta	tct	gaa	gga	tat	ctt	gaa	144
Met	Ser	Tyr	Ile	Ala	Ser	Asn	Gln	Ser	Leu	Ser	Glu	Gly	Tyr	Leu	Glu	
		35				40					45					

cag	gta	att	gtt	caa	tta	aag	aaa	aaa	ggg	ctt	att	aat	gct	aca	aaa	192
Gln	Val	Ile	Val	Gln	Leu	Lys	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Thr	Lys	
	50					55					60					

ggg	cca	ggg	ggg	ggg	tat	tca	cta	agt	att	gct	cct	cat	tta	att	aca	240
Gly	Pro	Gly	Gly	Gly	Tyr	Ser	Leu	Ser	Ile	Ala	Pro	His	Leu	Ile	Thr	
65					70					75				80		

ctt	agt	ctt	ata	ctt	gaa	tca	ata	ggc	gaa	aat	att	aaa	att	aca	aga	288
Leu	Ser	Leu	Ile	Leu	Glu	Ser	Ile	Gly	Glu	Asn	Ile	Lys	Ile	Thr	Arg	
				85					90					95		

tgc	gaa	aat	aac	agt	cca	ggg	tgt	cta	tcg	aat	aat	aat	aga	tgt	gta	336
Cys	Glu	Asn	Asn	Ser	Pro	Gly	Cys	Leu	Ser	Asn	Asn	Asn	Arg	Cys	Val	
			100					105					110			

act	cac	aaa	tta	tgg	gat	gat	ata	gga	aat	tat	ata	aaa	gat	tat	tta	384
Thr	His	Lys	Leu	Trp	Asp	Asp	Ile	Gly	Asn	Tyr	Ile	Lys	Asp	Tyr	Leu	
		115					120					125				

aat	aat	att	tca	cta	gag	gat	ata	gta	aat	aat	aat	ttt	agg	tca	aac	432
Asn	Asn	Ile	Ser	Leu	Glu	Asp	Ile	Val	Asn	Asn	Asn	Phe	Arg	Ser	Asn	
		130				135						140				

ata	gca	cta	cat	aaa	aac	gag	gaa	ccc	tat	ata	tat	gct	gat	tac	aat	480
Ile	Ala	Leu	His	Lys	Asn	Glu	Glu	Pro	Tyr	Ile	Tyr	Ala	Asp	Tyr	Asn	
145				150					155					160		

tca	aca	tct	acg	ata	cta	cct	gaa	gta	aaa	tat	caa	ttg	aat	aat	tta	528
Ser	Thr	Ser	Thr	Ile	Leu	Pro	Glu	Val	Lys	Tyr	Gln	Leu	Asn	Asn	Leu	

165

170

175

tcc tat ata aaa tta tat aat cca tct tca ata cat aaa cta ggt caa 576
 Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln
 180 185 190

aaa aca aaa agt ata ata gaa gaa aca aga aac ata gct att aag caa 624
 Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln
 195 200 205

cta aat gca caa tat tat gat gta gtt ttt aca tcc tct ggt aca gaa 672
 Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu
 210 215 220

gca aac aat tta gtc atc aat agt aca tca gac tat aaa cat tta att 720
 Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile
 225 230 235 240

tct tct aca gaa cat cta tct att ata aaa tgt gct act aat gca gaa 768
 Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu
 245 250 255

tta ata cct gtt gat tct aat gga ata ata tgt cta aat gca ttg agt 816
 Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser
 260 265 270

agt ctt tta cat aag ttt aaa gat gac aaa ata cta gta tca gta atg 864
 Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met
 275 280 285

aca gca aac aat gaa act ggt gct att caa cca ata aaa aaa atc gta 912
 Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val
 290 295 300

gaa cta tca cat aaa ttt gga gca tta gta cac aca gat gcc ata caa 960
 Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln
 305 310 315 320

gcg tgt gga aaa atc cat ata gat att gaa gat tta gga gtt gat ttg 1008
 Ala Cys Gly Lys Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu
 325 330 335

tta aca ata tca tca cat aaa ctt ggc agc att gct gga gca gga gtg 1056
 Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val
 340 345 350

tta ttc ttt aat agc aaa aag ata aat ata aaa cct atg ata att ggt 1104
 Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly
 355 360 365

gga cat caa gag aaa gga tta aga gca gga act gaa aat gtt tta gcg 1152
 Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala
 370 375 380

ata tac tta tta tct ata tca ctt agt aat tta tat aaa tct ata aca 1200

20080511 15:00:00

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr
 385 390 395 400
 aag atg ctt ctt gtt gaa aaa tta aga aat aaa ttg gaa aat gaa ata 1248
 Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile
 405 410 415
 tta tct tta gtt cct aac gct caa ata ttt agt aga aat gtc gag aga 1296
 Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg
 420 425 430
 cta cca aat act agt tgt att tca atg cca aat gta aat agt gag att 1344
 Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile
 435 440 445
 caa gta ata agc ttt gac ata aaa aat att gca gta ggt aac ggg tca 1392
 Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser
 450 455 460
 gca tgt tcc aca gga gta gta gaa ccc tct cat gtg tta tct gca atg 1440
 Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met
 465 470 475 480
 ggg gta aat cag gag att gca aat aat tca ata agg att agc tta agt 1488
 Gly Val Asn Gln Glu Ile Ala Asn Asn Ser Ile Arg Ile Ser Leu Ser
 485 490 495
 cct gac act aca gat gag cat ata aga act ata gta aac tgt tgg tac 1536
 Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr
 500 505 510
 gaa ata tat aca cat aat caa gtg cat aaa tga 1569
 Glu Ile Tyr Thr His Asn Gln Val His Lys
 515 520

<210> 107
 <211> 522
 <212> PRT
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 107

Met Leu Ile Thr Ala Arg Leu Arg Tyr Ala Ile Met Phe Met Val Lys
 1 5 10 15

Leu Ala His Gly Leu Cys Thr Gln Gln Asn Lys Leu Gln Pro Val Arg
 20 25 30

Met Ser Tyr Ile Ala Ser Asn Gln Ser Leu Ser Glu Gly Tyr Leu Glu
 35 40 45

Gln Val Ile Val Gln Leu Lys Lys Lys Gly Leu Ile Asn Ala Thr Lys
50 55 60

Gly Pro Gly Gly Gly Tyr Ser Leu Ser Ile Ala Pro His Leu Ile Thr
65 70 75 80

Leu Ser Leu Ile Leu Glu Ser Ile Gly Glu Asn Ile Lys Ile Thr Arg
85 90 95

Cys Glu Asn Asn Ser Pro Gly Cys Leu Ser Asn Asn Asn Arg Cys Val
100 105 110

Thr His Lys Leu Trp Asp Asp Ile Gly Asn Tyr Ile Lys Asp Tyr Leu
115 120 125

Asn Asn Ile Ser Leu Glu Asp Ile Val Asn Asn Asn Phe Arg Ser Asn
130 135 140

Ile Ala Leu His Lys Asn Glu Glu Pro Tyr Ile Tyr Ala Asp Tyr Asn
145 150 155 160

Ser Thr Ser Thr Ile Leu Pro Glu Val Lys Tyr Gln Leu Asn Asn Leu
165 170 175

Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln
180 185 190

Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln
195 200 205

Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu
210 215 220

Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile
225 230 235 240

Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu
245 250 255

Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser
260 265 270

Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met
275 280 285

Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val
290 295 300

Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln
305 310 315 320

Ala Cys Gly Lys Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu
325 330 335

Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val
340 345 350

Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly
355 360 365

Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala
370 375 380

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr
385 390 395 400

Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile
405 410 415

Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg
420 425 430

Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile
435 440 445

Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser
450 455 460

Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met
465 470 475 480

Gly Val Asn Gln Glu Ile Ala Asn Asn Ser Ile Arg Ile Ser Leu Ser
485 490 495

Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr
 500 505 510

Glu Ile Tyr Thr His Asn Gln Val His Lys
 515 520

<210> 108
 <211> 1242
 <212> DNA
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
 <220>
 <221> CDS
 <222> (1)..(1242)
 <223> Corresponds to SEQ ID NO:105, nucleotides 2099..3340
 Hypothetical iron-sulfur co-factor synthesis
 Product = "11hworf2"

<400> 108
 atg gaa aaa ata aaa gat ata caa cga cat att aat cta cct ata ttt 48
 Met Glu Lys Ile Lys Asp Ile Gln Arg His Ile Asn Leu Pro Ile Phe
 1 5 10 15
 ctt gat tat caa tcc aca act aaa acg gat agt aga gtc tta gat gct 96
 Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala
 20 25 30
 atg att cca tat ttt caa gag ttt tct aat cct cat tca cgt agt cat 144
 Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His
 35 40 45
 tgt ttt gga tgg aaa gct gag tcg gct gtt gaa tta gca cga gaa aga 192
 Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg
 50 55 60
 att gca tct tta ata aat gct gaa agt aaa gaa gta ata ttc act tct 240
 Ile Ala Ser Leu Ile Asn Ala Glu Ser Lys Glu Val Ile Phe Thr Ser
 65 70 75 80
 ggt gct aca gaa tca aat aat ttg gca att aaa ggt gta gca aac ttt 288
 Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe
 85 90 95
 tat aaa agt aaa gga aat cac att att aca gta cgt aca gag cat aaa 336
 Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys
 100 105 110
 tgt gtt tta gat tca tgt cgc cat tta gaa aca gaa gga ttt gac gtt 384
 Cys Val Leu Asp Ser Cys Arg His Leu Glu Thr Glu Gly Phe Asp Val
 115 120 125

act tac tta gat gta caa aaa aat ggt att tta gat ctt aat tta tta 432
 Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu
 130 135 140

aaa tca gct ata act gat aag act ata ttg gta tcg gtt atg atg gta 480
 Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val
 145 150 155 160

aac aat gaa att ggt gtc att caa cca ata gag gaa ata gga aaa att 528
 Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile
 165 170 175

tgt cat aat cat gga gta ttc ttt cat act gat gca gct caa gca ttt 576
 Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe
 180 185 190

ggt aaa ata cca ata gat gta aac aaa atg aat ata gat ttg ctt agt 624
 Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser
 195 200 205

ata tca gga cat aaa ata tat gct cca atg gga ata ggg gca tta tat 672
 Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr
 210 215 220

gta cgt aaa cgt caa cca aga ata cga ctt act cct ata ata aat ggt 720
 Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly
 225 230 235 240

ggt gga caa gaa cgt ggt atg aga tct gga acc ata cct act cca tta 768
 Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu
 245 250 255

gca gta ggt tta ggg gaa gca gca tat ata gct cag gaa gta atg gaa 816
 Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu
 260 265 270

gat gaa gcc att agg ata aaa gaa ttg cgt gat att tta tat agt gaa 864
 Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu
 275 280 285

ata aaa aaa cat tta ccc tat gta ata ctg aat ggt gat tat gaa caa 912
 Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln
 290 295 300

cgt ata gca gga aat tta aat tta agt ttt cca tat gta gaa gga gaa 960
 Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu
 305 310 315 320

tct att att atg gcg att aac aac tta gca gta agt tca gga tct gct 1008
 Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala
 325 330 335

tgt aca tct gct tca cta gaa cca tct tat gtt tta cgt gcg tta aat 1056
 Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn

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<210> 109
<211> 413
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 109

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Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala
20 25 30

Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His
35 40 45

Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg
50 55 60

Ile Ala Ser Leu Ile Asn Ala Glu Ser Lys Glu Val Ile Phe Thr Ser
65 70 75 80

Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe
85 90 95

Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys
100 105 110

Cys Val Leu Asp Ser Cys Arg His Leu Glu Thr Glu Gly Phe Asp Val

115

120

125

Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu
 130 135 140

Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val
 145 150 155 160

Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile
 165 170 175

Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe
 180 185 190

Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser
 195 200 205

Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr
 210 215 220

Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly
 225 230 235 240

Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu
 245 250 255

Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu
 260 265 270

Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu
 275 280 285

Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln
 290 295 300

Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu
 305 310 315 320

Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala
 325 330 335

200220 T503800T

Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn
340 345 350

Ile Asp Lys Asp Leu Glu His Ser Ser Ile Arg Phe Gly Ile Gly Arg
355 360 365

Phe Thr Thr Lys Ala Glu Ile Leu Tyr Ala Ala Asp Leu Ile Val Asn
370 375 380

Ser Ile Lys Arg Leu Arg Glu Met Ser Pro Leu Trp Glu Met Val Gln
385 390 395 400

Glu Gly Ile Asn Leu Asn Glu Ile Lys Trp Asp Val His
405 410

<210> 110

<211> 414

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(414)

<223> Corresponds to SEQ ID NO:105, nucleotides 3375-3788
NIFU-like protein
Product = "11hworf3"

<400> 110

atg agt tac agt gag tct ctt cta gaa cat tat aag aat cct aaa aat 48
Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn
1 5 10 15

gtt ggt act tta cct aaa gag gat tac aat gta ggt act ggc tta gtg 96
Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val
20 25 30

gga gct cct agc tgt ggt gat gta atg aag tta cag att aaa gta gat 144
Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp
35 40 45

gat aat gga aaa att ata gat gca aaa ttt aaa act ttt gga tgt ggt 192
Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly
50 55 60

gct gca att gca gct agt tca cta gct act gag tta att aaa ggt aaa 240
Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys
65 70 75 80

aca gta gat gag gca cat gag ttg aaa aat aca gta ttg gca aaa gaa 288

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu
85 90 95

tta agt tta cct cca gtg aaa ata cat tgt tca tta ctt gca gaa gat 336
Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp
100 105 110

gct gta aaa gca gct ata aat gac tat cat atg aaa caa gca aac aaa 384
Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys
115 120 125

aaa aat gct act aaa gat cct aat gaa taa 414
Lys Asn Ala Thr Lys Asp Pro Asn Glu
130 135

<210> 111

<211> 137

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 111

Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn
1 5 10 15

Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val
20 25 30

Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp
35 40 45

Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly
50 55 60

Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys
65 70 75 80

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu
85 90 95

Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp
100 105 110

Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys
115 120 125

Lys Asn Ala Thr Lys Asp Pro Asn Glu
130 135

<210> 112
<211> 15
<212> PRT
<213> Unknown

<220>
<223> Hypothetical sequence

<400> 112

Pro Thr Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
1 5 10 15

<210> 113
<211> 13
<212> PRT
<213> Unknown

<220>
<223> Hypothetical sequence

<400> 113

Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
1 5 10

<210> 114
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 114
cggggtaccg aattcctc

18

<210> 115
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 115
gcatgctcct ctagactc

18

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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 116

Val Thr Ser Ser Pro Glu Gly Ser Val
1 5

<210> 117
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<220>
<223> Synthetic peptide

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Val Thr Ser Ser Pro Glu Gly Ser Val
1 5

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